BIODISTANCE EVIDENCE FOR MIGRATION AND GENE FLOW IN THE NORTH AMERICAN SOUTHWEST, 2100 BC–AD 1700

by

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As members of the Dissertation Committee, we certify that we have read the dissertation prepared by ***Rachael Byrd***, titled ***Biodistance Evidence for Migration and Gene Flow in the North American Southwest 2100 BC–AD 1700*** and recommend that it be accepted as fulfilling the dissertation requirement for the Degree of Doctor of Philosophy.

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DEDICATION

This dissertation is dedicated to my husband Michael.

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ABSTRACT

The research presented in this dissertation develops a multi-scalar approach to reconstructing population histories from phenotypic variation in cranial morphology across the North American Southwest over time. One of the prime contributors to phenotypic variation in the region was migration. When considering the frequency of events and distances humans migrate, Native groups in the North American Southwest show considerable diversity in their trajectories. Archaeological evidence identifies substantial variation in locally-based and long-distance migration across the region prior to AD 1696. A great deal of research has focused on delineating the dimensions of migration to understand their impact on local and migrant communities; however, migration as a process involves both social and biological factors that require a heavily integrated approach to understand their effects on past populations. Therefore, it is important to identify the biological consequences (signatures) of population interactions to properly test archaeological models of migration.

In this dissertation, I take a population history approach at several scales to explore phenotypic variation in cranial morphology representing 3,800 years of occupation in the Southwest. I apply biological distance (biodistance) methods in a series of three analyses to reconstruct population histories, test archaeological migration inferences, and develop a framework for applied bioarchaeology in the region. The first study focuses on finer phenotypic variation, using three-dimensional measurements from the temporal bone, to test the proposed direct migration of people from the Kayenta region to pueblos and compounds south of the Mogollon Rim, and identify if co-residence of migrants within local communities led to gene flow and admixture. Samples included in this study consist of 204 individuals from the Kayenta region and several large Mogollon region pueblos (Turkey Creek, Point of Pines, and Grasshopper). Results demonstrate that the pre-migration Kayenta population is closely related to individuals from the earliest Point of Pines Pueblo site. Canonical Variates Analyses (CVA), both including and excluding migrants (identified through burial position, cranial modification, and isotope analyses), show minimal change in variation indicating that extensive gene flow occurred alongside co-residence.

The second study incorporates an extensive (temporally and geographically) craniometric database for the region to test for biological traces of four archaeologically-based migration processes: 1) colonization of open landscapes, 2) internal frontiers, 3) diaspora, and 3) coalescence and reorganization (following Mills 2011). Relethford-Blangero analyses, calculated using facial measurements from 1,299 crania representing 28 geographically and temporally defined sub-regions, provide support that biological signatures (morphological affiliation and variation) follow these migration processes in the region. The cumulative impacts of migration ultimately transformed, and had lasting effects on population structure and social organization across the North American Southwest. A significant amount of heterogeneity characterized how groups were structured and, along with biological affiliation, distinctive migration patterns are reflected in group variance.

The third and final study aims to develop a customized reference database—the Arizona Biological Affiliation Database (or AzBAD)—to aid in the integration of biological evidence into cultural affiliation or cultural affinity determinations pursuant to the Native American Graves Protection and Repatriation Act (NAGPRA) and Arizona state repatriation statutes. AzBAD also incorporates the extensive craniometric database developed through the second study but employs the commonly used forensic classification software Fordisc 3.1. This tool is then tested using a case study, the remains of an archaeological individual (including a cranium)

with limited contextual information, against the reference database. The resulting estimated biological affiliation highlights the importance of understanding local population histories of reference groups within the database to appropriately interpret biological affiliation for engaging and consulting with descendent communities.

Overall, the results of these studies clarify how evidence from cranial morphology and phenotypic variation can be aligned with archaeological inferences to formulate a more comprehensive understanding of migration as multiple interrelated processes with predictable biological outcomes. This research has archaeological implications as it directly tests migration inferences made from archaeological materials with biological evidence. In addition, tools such as AzBAD can contribute to the incorporation of biological evidence into consultations with descendant communities regarding ancestral human remains, and support bridging approaches to understanding the biocultural impact of population histories through time.

CHAPTER 1: INTRODUCTION

1.1 Overview and Hypotheses

The research presented in this dissertation develops a multi-scalar approach to reconstruct population histories over time from phenotypic variation and affiliation in cranial morphology across the North American Southwest (pre-AD 1696). This region provides considerable ethnographic and archaeological evidence of human migration across over 3,800 years of agricultural settlement (Bernardini 2005; Clark 2001; Duff 2002; Eckert 2008; Lyons 2003; Naranjo 1995; Ortman and Cameron 2011; Spielmann 1998). This study expands upon regional migration studies by testing archaeological inferences and models that are intrinsically tied to microevolutionary processes such as gene flow and genetic drift with multivariate analyses of cranial morphology.

Human migration impacts the genetic and social composition of local and regional human populations. Implementing approaches to understanding migration as an integrated social and biological process is necessary to move work on migration of past societies forward (O'Rourke 2012). Within the past decade, there has been a resurgence in regional scale studies of cranial morphology focused on subsets of past populations to test archaeological questions (Byrd 2014; Nikita et al. 2012; Schillaci and Stojanowski 2005; Von Cramon-Taubadel and Pinhasi 2011; Zakrzewski 2011). This dissertation explores cranial morphology at different scales in order to test long standing inferences of human migration in the Southwest.

In this dissertation, I take a population history approach at several scales to explore phenotypic variation in cranial morphology representing 3,800 years of occupation in the Southwest. I apply biological distance (biodistance) methods in a series of three analyses to reconstruct population histories, test archaeological migration inferences, and develop a

framework for applied bioarchaeology in the region. My first dissertation article (Appendix A) tests the hypothesis that co-residence and gene flow occurred after diaspora from the Kayenta area into large pueblos south of the Mogollon Rim. My second dissertation article (Appendix B) is broader in scope and tests four archaeological migration processes within three regional temporal periods, in order to reconstruct how these processes impacted biological affiliation and variation through time. My third dissertation article introduces the Arizona Biological Affiliation Database (AzBAD) as a tool developed to estimate biological affiliation of archaeological human skeletal remains to more effectively integrate biological evidence into the cultural affinity and cultural affiliation determination process in Arizona specifically, and across the Southwest region. A population history approach allows for integration of social and biological evidence to better track local and regional migration processes, and thus more effectively apply this information in consultation with descendent groups to support more holistic determinations of cultural affiliation. In addition, I revisit the measurement of cranial morphology as a biologically valid and accessible technique to help understand the impacts of migration in order to reconstruct population histories by integrating archaeological and biological evidence.

1.2 Materials

Geometric morphometric and linear measurements of human skeletal remains from the North American Southwest dating between 2100 BC–AD 1700 are the primary foci of the three studies included in this dissertation. Adult (age 18+ years of age) male and female individuals comprise this comprehensive regional sample. In addition, variables including site, burial ID, site location, site occupation date range, and sex were also compiled. These studies are multi-scalar with Article 1 focusing on phenotypically conservative, three-dimensional measurements from

the temporal bone and individual site-groups, whereas Articles 2 and 3 focus on higher levels of variation using a subset of facial measurements to compare temporally and geographically defined sub-regions. The first study includes the well-preserved left temporal bones of 204 adults representing site group samples of those buried at Black Mesa sites (in northeastern Arizona), Turkey Creek, Point of Pines, and Grasshopper pueblos (in central and southern Arizona). Only those with 10 landmark coordinates observable were included in the analysis briefly described in the following methods section.

For the second and third studies, individuals were grouped into temporal (Early, Middle, Late) groups and sub-regions. Sub-regions were defined by river and tributary drainages, geographic features, including the Sonoran Desert and Arizona Mountains, and current state political boundaries, such as Northeastern Arizona and Central New Mexico. For Article 2, eight craniofacial measurements were collected and compiled from 1,299 crania representing 28 sub-regions across the North American Southwest spanning 3,800 years of occupation. These data consist of standard linear cranial measurements collected by the author, compiled from numerous publications, and graciously shared by other analysts. For the third and final study eleven geographically and temporally defined Southwest groups represented by 1,841 individuals (927 females, 877 males, and 37 unidentified) were imported as a customized reference database into the forensic classification software, Fordisc version 3.1.

I, along with my co-authors, recommend a process for assessing cranial morphology from human remains with little or no contextual information. We identify statistical assumptions of this process as outlined by the developers of Fordisc, a widely-used forensic software. Finally, we test the utility of the database and its associated approach with a case study. Some argue that samples of human remains represent time-transgressed genetically cohesive lineages, or multiple

related generations within a community rather than a true population sample (Konigsberg 1990; Schillaci 2003; Stojanowski and Schillaci 2006). They are essentially diachronic burial samples that represent the comprehensive phenotypic variation present in all lineages buried within the defined sites and sub-regions. Although these studies focus on the variation and affinity among a limited number of people who are assumed to represent site group samples, sub-region samples, and the regional Southwest population, archaeological and bioarchaeological studies in the region need to incorporate available morphological evidence to understand how people were related, migrated, and organized themselves in the past.

1.3 Methods

Three different methods for examining phenotypic variation through cranial morphology were utilized along with three separate sets of statistical analyses. For my first study, temporal shape is measured by using 10 coordinate landmark points on the left temporal with a Microscribe 3DX digitizer (Immersion Corporation, San Jose, CA, USA). Each temporal was positioned on a set of three hand-made clay pillars to provide stability and allow for data collection from all angles and positions. Coordinate landmark points collected focused on the petrous portions which house the inner ear, locations of nerves and arteries, and external auditory meatus dimensions. Data processing and analyses were conducted in MorphoJ (Klingenberg 2011). Generalized Procrustes Analysis (GPA) was the first step used to rotate, translate and scale landmark coordinate points to remove size differences and make them comparable (Mitteroecker and Bookstein 2009). This process allowed for the pooling of male and female crania to maximize sample sizes. Multiple analyses were conducted to test the proposed hypotheses.

Article 1 (Appendix A) uses covariance matrices to calculate Procrustes coordinates in order to test biological affiliation among samples from the Kayenta area of northeastern Arizona and large pueblos south of the Mogollon Rim including Point of Pines, Turkey Creek, and Grasshopper pueblos. Covariance matrices were then subject to Principal Components Analysis (PCA) to reduce dimensionality through ordination of shape variance by identifying the linear combination of maximum variance to summarize the variability (Slice 2007; Lawing and Polly 2010). Canonical Variates Analysis (CVA) was then used to calculate linear functions associated with canonical correlations between sets of variables and to classify two or more groups that best represent variation in the total sample (Cooke and Terhune 2015; Rencher 1992). Since matrices violate the statistical assumptions of traditional correlation tests, computed Mahalanobis biological distance and Procrustes matrices were statistically compared used Mantel tests, with p-values assigned following randomization using 10,000 permutation. Results are presented as distance matrices (geographic, Procrustes, and Mahalanobis) for the Kayenta, Turkey Creek, Point of Pines, and Grasshopper site-groups including, and excluding migrants, which were previously identified through burial position, cranial modification, and isotope studies (Ezzo et al. 1997; Rodrigues 2008). Scatterplots were used to help visually represent biological affiliation and variation patterns among these settlements.

Article 2 (Appendix B) utilizes standardized linear (Euclidean) cranial measurements (manually collected and compiled from publications, reports, and personal communications) to test three archaeological migration models. Eight facial measurements were selected and compiled from 1,299 individual crania recovered from Southwest archaeological sites representing 28 geographically and temporally defined sub-regions. Early (2100 BC–AD 500), Middle (AD 700–1400), and Late (AD 1100–1700) periods were used to categorize sub-regions

and provide limited temporal control. Cranial measurements along with associated variables including sub-region, site, burial identification, and sex were organized into a database. Multiple imputation was performed with an algorithm based on the Markov Chain Monte Carlo to obtain missing measurement values taken from the normal distribution, before z-score standardization which allowed for the pooling of males and females. The Relethford-Blangero (1990) analytic model, with phenotypic variation and biological distances calculated based on standardized craniofacial measurements and a priori designated groups is applied in my second article to test the four proposed archaeological migration processes in the Southwest within three time periods. Relationship matrices (R-matrices) are used to produce measures of Wright's F_{ST}, or population differentiation (Relethford and Harpending 1994). Distance matrices (D-matrices) are converted from unbiased R-matrices, and Mantel tests calculated with PaSSaGe software to test biological distance correlation with geographic distance (Rosenberg and Anderson 2011). These analyses allow for the examination of biological affiliation patterns in order to test the proposed archeological migration models.

Article 3 (Appendix C) presents a regional reference database composed of 34 standardized cranial measurements collected by the authors following descriptions listed in Buikstra and Ubelaker (1994: 74–78). Additional data were provided by other analysts and compiled from published reports, dissertations, and archival documents. Of these, 15 facial measurements were identified to be included in the initial analysis, but as following sections address, only eight of these were ultimately used in the biological affiliation analysis. Linear Discriminant Function Analysis (LDFA), leave-one-out cross validation (LOOCV), and typicality and posterior probabilities were calculated to test the closest biological affiliation of a case study with limited associated contextual information, and to demonstrate how to use a

regionally customized database for providing biological affiliation evidence. These calculations were conducted in Fordisc 3.1, using a case study with limited associated context. This study supports the conclusion that biological integration likely did occur alongside co-residence but at different degrees and through different processes in the pre-contact Southwest.

The three studies presented in this dissertation address the impacts of migration on multiple scales, and each provides a different perspective based on the proposed hypotheses and archaeological models and inferences tested. Knudson and Stojanowski (2008) assert that biodistance is an analytic approach in bioarchaeology that articulates with the study of past social identities, yet it is not simply about who is related to whom, but more so about how relationships changed through time along with the potential significance of increasing or decreasing biological integration through the lens of social organization. Conversely, Armelagos and Van Gerven (2003) have previously described biodistance as an approach that lacks development, argued that past relationships described in terms of biological relatedness are irrelevant, and suggested that the approach is solely typological in nature. This position is challenged with the multi-scalar population history approach presented here, consisting of three consecutive studies intentionally designed to test long-held archaeological inferences of migration in the Southwest.

1.4 Organization of Dissertation

Three dissertation articles are included as appendices. The first article, *Biodistance Evidence of Gene Flow from the Kayenta Region* (Appendix A) tests if gene flow followed the socioeconomic upheaval and environmental fluctuations that motivated people to move out of the Kayenta region of Northeastern Arizona to large pueblos south of the Mogollon Rim. Landmark coordinate points were collected from the left temporal of individuals from Black

Mesa sites, Turkey Creek, Grasshopper, and Point of Pines pueblos. Results indicate that all groups except for Point of Pines Pueblo exhibit significant distances from each other, which corresponds with archaeological inferences. Gene flow occurred between Kayenta region migrants, their descendants born in the Points of Pines region, and people at earlier Black Mesa sites representing a pre-migration population. Grasshopper Pueblo was occupied by people with diverse origins with some evidence of some gene flow and community integration across the region, but also from areas not included in this analysis. Migration, co-residence, and admixture ultimately led to widespread gene flow that occurred variably in large pueblo communities south of the Mogollon Rim.

The second dissertation article (Appendix B), entitled *Reconstructing Population Histories Using Biological Distance across the North American Southwest (2100 BC–AD 1700),* tests affiliation and variance expectations of four migration processes within three temporal periods derived from archaeological evidence: [1) colonization of open landscapes, 2) internal frontiers, 3) diaspora, and 4) coalescence and reorganization] (following Mills 2011). By applying the Relethford-Blangero analytic method, phenotypic variance and biological distances were calculated among geographically and temporally defined sub-regions within the Southwest spanning 3,800 years of agricultural occupation. By taking a population history approach this study explores how different migration processes dynamically impacted the biological composition of agricultural communities across space and time.

An applied approach was taken with the third article, *Integrating Biological Evidence into the Cultural Affiliation Process in the Southwest* (Appendix C), by constructing a large biological affiliation reference database called AzBAD. This reference tool is for use in Arizona and throughout the North American Southwest to support the integration of biological evidence

into the process of determining cultural affinity or affiliation. Customized reference databases show promise for testing regional biological affiliation across the Southwest and this study serves as a model for how to apply such databases with similar goals across the United States in compliance with NAGPRA and related state statutes. This study highlights the importance of considering population history and the complicated migration processes that affected human biological and cultural variation in the North American Southwest when interpreting morphological affiliation.

1.5 Broader Impacts

Migration transform communities and this research demonstrates how phenotypic variation, as measured through cranial morphology, can have implications for diachronically tracking migration processes within a population history framework. Migration can have differential effects on population structure at local and regional levels through gene flow. The archaeological implications for this work are directly tied to testing inferences of migration made from archaeological materials with methods that designed for use with standardized cranial measurements.

Standard cranial measurements are widely collected by bioarchaeologists, biological anthropologists, and forensic anthropologists when documenting and working with human remains. As more measurements are collected, more regionally representative reference samples become available for biodistance studies drawing from the methods presented here.

By bridging these fields, more informed and holistic inferences on past migration can be tested. This work moves away from typological and cultural group comparisons and focuses specifically on broadly defined temporal and geographic sub-regions. Taking this perspective

allows for studying the effects of microevolutionary processes, such as gene flow and genetic drift, had on local and regional human groups. Related fields such as anatomy and evolutionary biology, for example, focus heavily on how human cranial function impacts shape. This work emphasizes that layered shape variation due to specific socially directed migration processes must also be considered within frameworks of natural selection and plasticity when explaining observed skeletal variation.

Determining cultural affiliation as defined by NAGPRA has promoted increased engagement between anthropologists and descendant communities. This, in turn, has resulted in heightened understanding of how social, and as I argue, biological identities, are closely connected with migration processes and past population histories (Cameron and Ortman 2017). Tools such as AzBAD help facilitate this process in order to provide the most information available to descendent communities to aid in cultural affiliation determinations. Biological anthropology's role within the cultural affiliation process is not to overemphasize the biological line of evidence, but to provide as much information as possible to Native American tribes and descendant communities (Colwell-Chanthaphonh et al. 2011). This work provides a framework for how to use such tools in other regions of the US to support the NAGPRA process. Further efforts into understanding the links between present and past Native American groups through non-destructive methods can help balance the needs and rights of descendent groups, legislative mandates, and scientific approaches to help increase understanding of human diversity and preserve heritage.

1.6 Future Directions

Intermarriage, migration, and admixture built and maintained social and economic networks, defense alliances, community cooperation, and solidarity across the Southwest in the past (Stodder 2006). Research on prehistoric post-marital residence patterns using craniometric data assume that gene flow causes distinctive levels of variance between males and females attributed to different levels of exogamy (out migration) (Konigsberg 1988; Lane and Sublett 1972; Schillaci and Stojanowski 2005; Spence 1974; Steadman 2001). Ensor (2013) suggests expanding biodistance studies conducted in the Southwest to encompass multiple population samples to help elucidate the level of male and female exogamy and endogamy and how these choices influenced social organization. Post-marital residence patterns refer to the social rules and practice of where a married couple chooses to live (Divale 1974; 1977). They are intrinsically tied to human movement, migration, and settlement patterns of males and females after marriage, and reflect a small scale source of variation related to larger regional patterns. Pasternak et al. (1997) states that post-marital residence is important because it determines how people live, with whom they cooperate, and upon whom they rely on. Cross-culturally, patrilocality, where women leave their natal groups and reside with the husband's family, is most common (Ember and Ember 1971, 1972; Murdock 1967). Competitive interaction and resource pressure with other societies is thought to influence the transition to matrilocal residence (Divale 1974; Peregrine 2001). Biodistance studies can help address post-marital residence patterns with the assumption that where an individual is buried reflects post-marital residence in association with all other individuals at that site (Schillaci and Stojanowski 2005; Stojanowski and Schillaci 2006). The data collected for this dissertation will be used in future studies to examine patterns of affiliation and variation between males and females to infer patterns and trends across the

region in order to provide further insight into how this type of movement impacts group organization and is reflected in morphological affiliation.

CHAPTER 2: LITERATURE REVIEW

2.1 Theoretical Approaches to Migration in the Southwest

Migration as an anthropological focus formed within the cultural-historical approach as an explanation for culture change, or replacement (Childe 1956; Trigger 1996). The cultural historical approach was popularized in North America in the first half of the twentieth century which focused on the mechanisms of migration and diffusion causing culture change identified from cultural traits (Cameron 1995). While migration involves the physical movement of people ushering in change, it can also result in diffusion, or the spread of cultural traits through trade or emulation. Often abrupt changes in the material record were interpreted as being the result of migration. Early archaeologists in the Southwest are described as using a "direct-historical" approach to inferring migration from archaeological evidence (Fewkes 1904; Steward 1942). These archaeologists looked at ceramics, architectural style, and oral traditions often linking past ancestral sites to modern Puebloan people (Cushing 1890; Fewkes 1904; Kidder 1924).

Haury (1958) proposed a model for identifying migrants with archaeological evidence through his work at Point of Pines pueblo. He sets forth conditions needing to be met in order to infer if migration occurred from archaeological evidence. One condition proposed includes identifying migrant intrusion through distinguishing material characteristics that are new and without local prototypes. The second condition of interaction is achieved if the characteristics of migrant groups reflect borrowed elements from local groups along with preserved material aspects associated with their origin location. However, application of Haury's model may be limited on the regional scale as distances moved can be short, with migrations of small groups, which may result in a lack of clearly distinguishable boundaries (Mills 1998).

Clark and colleagues (2013: 400) define migration in non-complex societies as "long-term residential relocation by one of more discrete social groups across community boundaries in response to spatially uneven changes in social and economic conditions". Migration research can be divided into four categories, detection, motivation, organization, and impact (Clark 2001; Herr and Clark 1997). More recent material approaches to migration focus on variability in technological style, expressed in ceramics, architecture, and mortuary behavior (Carr 1995; Eckert 2008; Lyons 2003; Mills 1998; Neuzil 2008; Spielmann 1998). Clark (2001), in his study of migrants into the Tonto Basin, focuses on technological style to identify social boundaries. Low visibility material indicators of enculturation reveal more subtle learned manufacturing behaviors connected with origin areas. Push-pull factors motivating migration include environmental change and fluctuation, drought and famine, conflict and upheaval, and economic pressures (Anthony 1990; LeBlanc 1999; Lowell 2007).

Recent research has shifted from simplified considerations of migrant-host relations to modeling migration as coerced or unplanned, such as those occurring through warfare and captive taking, processes of fission and fusion, and random demographic events, against the logistical backdrop of duration and pace of movement, as well as group size and composition (Cameron 2013). Variables in contemporary migration research include causes, scale, and consequences of migration. Scale relates to, for example, the number of people involved, the distance they moved, and the span of time during which migration occurred. Preexisting connections between destination and host communities and the social consequences of migration are important foci of archaeological migration research (Ortman and Cameron 2011).

In the North American Southwest three models of migration are generally applied to processes inferred from settlement and material patterns. These include, 1) colonization of open

landscapes, 2) movement into internal frontiers, and 3) large-scale diaspora (Mills 2011:354–359). Movement into, and colonization of open landscapes occurs when highly mobile groups seek fertile land and ample resources in rapid migrations that cover wide expanses of territory (Barton et al. 2004; Goebel et al. 2008). Although describing this movement as colonization is contentious (Cameron 1995), here it is used to mean the establishment of a new home range (Ortman and Cameron 2011). Groups participating in such migration carry only a subset of the biological and cultural variation present in their natal homelands (Anthony 1990; Bellwood 2013). As migrant populations grow, they can become substantially differentiated from their natal population as time passes. This form of migration lays the foundation for subsequent long-distance point-to-point migrations from one occupied settlement to another (Anthony 1990; Mills et al. 2016).

As agricultural communities became more densely populated over time and resources became more constrained, people dispersed into more sparsely occupied areas referred to as internal frontiers (Herr 2001; Kopytoff 1987; Ogundiran 2014; Schlegel 1992). Politically open areas located between organized settlements (Cameron 1995) serve as buffer zones, zones of expansion, and as transition zones across trading and political networks (Ogundiran 2014). Fertile land and economic opportunities likely were the pull factors motivating decisions to move into and form new communities within internal frontiers. Diaspora occurs as the result of crises and upheaval that push people to move and re-settle a long distance from their natal homelands into already occupied settlements (Clifford 1994; Cohen 1997). Lateral connections and networks are generally maintained among diasporic communities (Cohen 1997).

Safran (1991) describes diasporas as consisting of expatriate communities that maintain traditional ties to their homeland, have a history of dispersal into multiple locales, and an

ideology of return that shapes their collective identity. Migrant groups are small but are part of the much larger diaspora process. Important characteristics of diaspora include, relatively large population displacement, maintenance of network connections and aspects of identity, zones of heterogeneity, and the ultimate transformation of local population histories and trajectories (Mills 2011). Population upheaval and relocation requires reorganization when migrants co-reside with local inhabitants. Coalescence is a term applied to this process that refers to community reorganization and the reformation of diverse aggregated groups (Hill et al. 2004; Kowaleski 2003). Migration is a catalyst for coalescent communities to form, as it generates economic pressure and social disruption, often at a large scale (Hill et al. 2004). In this way, social reorganization found in coalescent communities brings diverse people in contact where they then have increased opportunities to co-reside and reproduce, which in turn affects the structure and organization of the community overtime.

Oral traditions of the Native peoples of the Southwest include migration stories that recount group origins in distinct locations, as well as movement through transitional places, and are linked to group identities (Bernardini 2008; Bernardini and Fowles 2011; Duff 2002; Ferguson 2007; Naranjo 1995). NAGPRA promotes engagement with Native American tribes as it requires oral tradition be considered within the cultural affiliation process which, in turn, aids in understanding the importance of movement and migration in the Southwest (Cameron and Ortman 2017).

Demographic variables such as birth rate and population size are directly influenced by migration. Demographic studies indicate that over a 500-year time range (AD 500–1000) populations had steadily increasing birth rates with some fluctuation until AD 1300, when they began to decline (Hill et al. 2004; Kohler and Reese 2014). As birth rates plateaued around AD

1000 in the Southwest, people sought to exploit smaller territories, or internal frontiers, as a viable option for population continuity (Kohler and Reese 2014). When reproductive-aged people migrate, they leave a population with older people and a decreasing birth rate. Kohler and Reese (2014) use measures of the juvenility index to estimate birth rates in the North American Southwest from 1100 BC through AD 1400/1450 and find that pre-Hispanic people experienced high rates from AD 500–1300 that peaked from AD 700–1200. The northern and southern Southwest show markedly different trends in juvenility indices, with the northern areas showing higher juvenility indices than the southern areas. A low juvenility index was found in the Tonto Basin and Verde Valley, whereas a high juvenility index was found in the Mogollon area. Juvenility indices declined gradually in the Middle Rio Grande from AD 1200–1500, whereas they fluctuated dramatically in the Northern Rio Grande during this time. Although multiple different factors can contribute to population size, migration impacts in the Southwest were so prevalent and differentiated over time that this region provides an ideal setting for testing corresponding biological impacts through cranial morphology. Extensive work has laid the foundation for analysis of the biological impacts of migration in the Southwest.

2.2 Biodistance Studies in the Southwest

Studies of cranial morphology in the Southwest have played a major role in the approach's theoretical and analytic trends and are particularly relevant to addressing questions of migration and biological connectivity in the past. One of the earliest studies conducted on the cranial morphology of Southwest groups was that of Earnest Hooton in 1930 on human skeletal remains from Pecos Pueblo, where he described morphological changes through five phases (AD 1315–1838). He argued that, throughout the phases, the Pecos Pueblo people became

increasingly homogenous. Ales Hrdlička (1931) published the first Southwest craniometric series, with data collected from numerous sites across the region that are included in this study. He presented conclusions arguing for two biological Puebloan groups, one he termed ‘dolichoid’, or long and narrow, and the other ‘brachyoid’, or short and wide. Specifically, he found Hawikku individuals to be the most dolichoid, Puye the most brachyoid, and Jemez to be intermediate. Ultimately, Hrdlička suggested that there were not physical subdivisions that corresponded with cultural taxonomies and that extra-regional people caused differences in cranial shape. In addition, he argued that the Puebloan group was heterogeneous and did not show affiliation with the Navajo.

Seltzer (1944) reassessed Hrdlička’s Southwest data and added Basketmaker and Rio Grande individuals into his craniometric comparison. He argued that all Southwestern groups are of the Basketmaker physical type and are biologically unified. His results also indicated that Puye was differentiated from the other groups, but he did not feel that the level of differentiation in morphology reflected the existence of a separate biological group. A little over a decade later, Neumann (1952) also supported the notion of a general Southwestern physical type, one that cannot be separated by site or tribe. Additionally, he provided some support for Hrdlička’s inference that external migration caused intermixed groups which complicated the inference that the Southwest region contained one biological group. Here two competing viewpoints surfaced in the early years of Southwest craniometric studies, 1) Ancestral Puebloans are a homogenous, continuous group; and 2) Ancestral Puebloans are heterogeneous due to admixture and assigned to hypothetical ‘types’ or groups.

Corrucini (1972) re-evaluated relationships between Hawikku, Pueblo Bonito, and Puye with three goals, 1) to ascertain the effects of Spanish colonialism on the Pueblo gene pool, 2) to

investigate if these groups could be lumped together as a single homogenous sample, and 3) to shed light on the problem of 'Southwestern racial prehistory.' At Hawikku, he found little divergence between early versus late (post-Spanish contact) groups at the site and suggested that they were likely one homogenous population. Furthermore, Corrucini (1972) argued that although Ancestral Pueblos form several statistical populations, they can also be treated as a single regional group for comparison with other regional groups. Additionally, he found that Puye exhibited little variation and was likely more of an isolated population with effects from selection and genetic drift (reducing variation) rather than migration and gene flow (that would have conversely increased variation). He inferred that genetic drift was the primary mechanism that effected the variation of Southwestern groups, more so than gene flow and directional selection.

Bennett (1973) analyzed skeletal remains from Point of Pines and found similarities between two temporal groups of people buried at the site outweighed the differences. He inferred that people living at Point of Pines were biologically homogenous, with morphology similar to Mesa Verde individuals. El-Najjar (1978) tested the biological affiliation (coefficient of divergence) of 15 groups from Canyon de Chelly, Gran Quivira, Hopi, Kayenta, Mesa Verde, Old Mission Zuni, Pueblo Bonito, the Sinagua area, Pecos, Point of Pines, Chavez Pass, Puye and the Salt River. He found that the Canyon de Chelly group was most similar to the Kayenta and Hopi groups and least similar to the Chavez Pass group. The largest coefficient of divergence was between the Mesa Verde and Pecos Pueblo groups. His study found that craniometric data were generally in agreement with the chronological divisions and cultural taxonomies of Southwest archaeologists. However, because El-Najjar (1978) defined groups

tested by both sub-region and site within the Southwest, relationships identified likely reflect site level affiliation with larger, more diverse sub-region samples.

Including groups from the eastern Southwest, Mackey (1977) did not find continuity between Gallina and Jemez groups when he tested to see if skeletal morphology followed an archaeological defined cultural continuum. He tested morphological continuity from the Los Piños and Arboles (AD100–1000), Largo Gallina (AD 1050–1300), and Jemez Vallecitos (AD 1300–1700) phases with 10 face and base standardized measurements. He did not find continuity between the phases and, therefore, inferred that the Largo Gallina individuals were not ancestral to the Jemez individuals. In addition, he inferred a large biological distance between Pecos and Jemez. He notes that Pecos was very distinct, and that it may be a "genetic isolate" (1977:481). His findings regarding Pecos Pueblo are in line with those reported by El-Najjar (1978).

In a study of biological relationships among the inhabitants of Chavez Pass pueblo, Elden pueblo, Grasshopper pueblo, Point of Pines pueblo, Turkey Creek pueblo, a group of sites in the Kayenta area, and Las Acequias, Miller (1981) calculates biological distance of modern day Eastern and Western Pueblo groups along with the Akimel O'odham (Pima) and Tohono O'odham (Papago). His results show morphological homogeneity, without correlation between biological and geographic distances between the groups. Additionally, Miller (1981) argues that pronounced morphological differentiation present today among modern Native groups indicates that these groups are more isolated now than groups were in the past. Shipman (1982) compared craniometrics among east-central Arizona pueblos, including Grasshopper, Kinishba, Point of Pines, and Turkey Creek. He used Pearson's Lambda Criterion and discriminant analysis and argues that the four groups were biologically homogenous.

The morphology documented as the result of Chaco Canyon cranial morphometric studies has undergone multiple interpretations. Akins (1986) finds two divergent skeletal populations at Pueblo Bonito, corresponding with north and west burial clusters, and Schillaci (2003) provides additional evidence of a diverse population buried in Chaco Canyon. His results show that Pueblo Bonito was most closely related to the Grand Gulch western Basketmakers (Basketmaker II). He suggests that there was either reduced migration from outside sources or increased genetic drift due to reproductive isolation and a small effective sample size for BC 51 and BC 53 relative to others in Chaco Canyon. Inferences suggest that the best model for the development of population diversity at Chaco Canyon being aggregation of regional populations, including the Cibola, La Plata, and Dolores population areas, with some gene flow from Rio Grande groups (Schillaci 2003).

Schillaci and Stojanowski (2005) assess cranial morphology of Otowi, Tsankawi, Puye, Sapawe, and San Cristobal for evidence of Tewa migration in the Northern Rio Grande. Using determinant ratio analysis, they examine genetic distances among and within Pueblos and heterogeneity. Their results do not find relationships between phenotype and geographic distance, supporting the conclusion that geography and distance were not the primary basis for gene flow. Using the Relethford-Blangero analysis, results show within-group heterogeneity indicating significantly high in-migration or gene flow from outside sources for Otowi and possibly San Cristobal. They suggest that Puye may have been matrilocal as there was higher male variation compared with female variation. Sapawe appeared to be a relative outlier, and they suggest Otowi might have been unique in terms of population history. This study supports the idea of diversity being present in the Northern Rio Grande rather than consistent population continuity.

In a more recent study, Minturn (2006) found evidence that the prehistoric inhabitants of the Tonto Basin in Central Arizona showed affinity in multiple directions. People from the Salt arm of the Tonto Basin were more closely affiliated with Hohokam people, whereas people from the Tonto arm were more closely affiliated with Archaic, Central Arizona, and Zuni populations. Her study suggests that people with multiple origins lived in the Tonto Basin, with distinct differences among the Classic period populations within the basin. She infers that because the Salt arm is geographically closer to the Lower Salt River Valley, Hohokam groups likely migrated into the Salt Arm, but few moved into the northern part of the Tonto arm. She asserts that the relative rarity of platform mounds on the Tonto arm also supports this inference.

Ortman (2010, 2012) argues that the ancestral Tewa people of the Northern Rio Grande migrated from the northern San Juan based on a biodistance analysis of populations in the Rio Grande, San Juan and Little Colorado drainages. His results show overlapping patterns of affinities among populations from different portions of the Pueblo region, confirming that Pueblo populations were relatively similar due to long-standing gene flow. Most post-AD 1275 groups of the Northern Rio Grande are more closely related to earlier groups from the Four Corners, compared with earlier groups from the Northern Rio Grande region. He makes a strong case that ancestral Tewa populations had origins in the northern San Juan. Peeples (2014) analyzed the population history of the Zuni region through a biodistance lens and finds that the protohistoric transition (AD 1450–1540) involved substantial immigration from multiple locations across the Southwest. He finds that at the protohistoric village of Hawikku that gene flow accounts for a portion of the genetic diversity at the site, but also that a relationship exists with earlier populations across the Zuni region.

Non-metric dental and DNA data analyzed within a biodistance framework provide insightful comparative results on the intra-site scale. For example, McClelland (2003) found patterns in cranial non-metric and dental non-metrics of Grasshopper pueblo people indicative of multiple residential groups at this large settlement, which is also aligns with strontium isotope studies that demonstrate people living at Grasshopper pueblo multiple origins (Ezzo et al. 1997). Durand et al. (2010), in a study of nonmetric traits in the Middle and Southern San Juan sub-regions, finds close relationships within and between the adjacent sub-regions.

Genetic studies are becoming increasingly prominent throughout the Southwest. Analyses of quids and aprons found in caves have led to inferences that western Basketmaker groups were migrants from Mexico who introduced maize agriculture in to the Four Corners area of the Southwest, and support the conclusion that western and eastern Basketmaker groups, the earliest farmers in the northern Southwest, had distinct origins (LeBlanc et al. 2007). Results presented in my second dissertation Article (Appendix B, Model 1) support this inference as cranial morphological signatures of Western Basketmaker groups from the western San Juan and northeastern Arizona show high affinity with those from the Sonoran Desert, and Eastern Basketmaker people from the northern San Juan (Early) sub-region exhibited very distinctive cranial morphology.

People from the Mimbres and Casas Grandes areas were not included within the sample for this study, although recent DNA studies of a limited number of individuals indicate that Mimbres people bear many similarities to people within the Southwest, yet their haplotype clusters more closely with Zuni and O'odham modern people suggesting possible gene flow and population continuity between these groups (Carlyle et al. 2000; Snow et al. 2011). Morales-

Arce et al. (2017) looked at aDNA and ancestry of inhabitants at Casas Grandes (AD 1200-1450) and found close affinity present between Casas Grandes and Mimbres people.

In a recent study of Chacoan DNA collected from 9 individuals buried in elite graves within Room 33 of Pueblo Bonito, identical mtDNA sequences between different pairs of individuals were identified (Kennett et al. 2017). These signatures are inferred to be traces of institutionalized hereditary leadership was passed through the female lineage at Pueblo Bonito, constituting a matrilineal dynasty that lasted approximately 330 years.

At the beginning of the 20th century, in the early years of Southwest craniometric studies, two competing viewpoints emerged: 1) Ancestral Puebloans are a homogenous, continuous group; and 2) Ancestral Puebloans are heterogeneous due to migration (gene flow) and genetic drift. As mid-20th century cranial research became more comprehensive and less typological, it was recognized that patterns of affiliation were present within the region on inter- and intra-site scales. However, before the turn of the century, almost all studies (except for Mackey [1977]) inferred homogeneity and continuity among the samples tested.

Previous studies that highlight heterogeneity, find that occupants of the Gallina region, Chaco Canyon, the Northern Rio Grande, and the Tonto Basin as have cranial morphology indicative of possible high in-migration, or gene flow from outside sources (Mackey 1977; Minturn 2006; Schillaci 2003; Schillaci and Stojanowski 2005). Currently, biodistance studies, whether focusing on cranial morphology, dental morphology, or DNA, are often used to test archaeological inferences, rather than provide overgeneralized descriptions and comparisons.

2.3 Cranial Morphology: Refining Theoretical Approaches

2.3.1 Heritability

It is widely agreed that human cranial morphology proportionately reflects genetic relationships due to moderate heritability, which allows it to be used as a proxy for reconstructing population histories (Carson 2006; Martínez-Abadías et al. 2006, 2009; Reyes-Centeno et al. 2017). Many factors impact the final adult cranial morphology, and biological distance (biodistance) studies apply parameters of narrow-sense heritability (between 0.0-1.0) used to reconstruct biological (phenotypic) affinity among groups included in the analysis. Narrow-sense heritability is the ratio of the additive genetic variance to the total phenotypic variance (Carson 2006; Falconer 1989). Estimation of narrow-sense heritability is a parameter included in the Relethford-Blangero analysis in Article 2 (Appendix B). Distinguishing microevolutionary trajectories as reflected in the heritable aspects of cranial morphology requires initially focusing on heritability levels specific to regional populations. Heritability levels are population specific, as both additive and non-additive genetic influences and environments encountered are also population specific (Visscher 2008). Although calculating heritability based on crania with associated genealogical data is theoretically ideal, the reality is that these data are not often collected or available.

Heritable aspects of the human cranium are found to be different across cranial regions defined by function, also referred to as modules, and include the face, vault or neurocranium, and base or basicranium. Smith (2009) found by examining the correlation of three-dimensional cranial morphometric and microsatellite data that the morphology of the temporal bone, upper face, basicranium, and entire cranium consistently reflect genetic relationships in humans. However, she suggests that with an international, modern cranial sample, the base and face are

significantly correlated with genetic data whereas the vault is not. Martínez-Abadías et al. (2009) assess heritability estimates using maximum likelihood (ML) methods and find that the human cranium exhibits substantial amounts of genetic variation and that there are not statistically significant different levels of heritability between cranial regions.

By correlating population affinity matrices, Von Cramon-Taubadel (2009) found that the temporal bone showed the strongest correlation with associated genetic data compared with other cranial bones tested, although not significantly more than the sphenoid, frontal, or parietal. The constrained development of the temporal bone closely follows the shape of the brain and the inner ear (Lockwood et al. 2002; Smith et al. 2013; Terhune et al. 2013). Therefore, it is argued that the temporal bone provides an ideal cranial element for tracking biological affiliation as it is found to closely coincide with neutral genetic distances. My first dissertation article (Appendix A) focuses solely on the left temporal bone, whereas articles 2 and 3 (Appendix B and C)examine facial and base morphology to reconstruct population histories in the North American Southwest.

2.3.2 Microevolutionary Effects

Cranial morphology is affected in three ways by migration: 1) changes in among group differentiation and genetic distance through gene flow and genetic drift, 2) movement into a different environment followed by natural selection and adaptation, and 3) movement into a different environment that leads to developmental plasticity (Relethford 2004). Over the past two decades, theoretical and methodological advances have confirmed that cranial morphological variation parallels genetic variation and thus, population history (Smith 2011; Von Cramon Taubadel 2009; Zichello et al. 218). Relethford (1996) defines population history as the inferred

pattern of ancestor and descendant relationships and evolutionary histories among populations and aims to reveal historical connections based on phenotypic similarity.

Population within- and between-group variation is directly affected by microevolutionary forces such as gene flow and genetic drift, more so than natural selection (Roseman and Weaver 2007). It is generally agreed that most of the variation present in human populations in within groups rather than between groups; an argument vehemently applied against the concept of biological human races (Lewontin 1972; Relethford 1994; Strauss and Hubbe 2009; Witherspoon et al. 2007). Recent studies address how time and geographical factors can also influence aspects of phenotypic relatedness and variation (Keita and Boyce 2008; Nikita et al. 2012; Relethford 1996).

Patterns in the variation of global cranial morphology fit expectations of iterative founder effects, with similarity between human groups decreasing the farther in distance they are located from sub-Saharan Africa (Betti et al. 2009; Manica et al. 2007). When populations exchange mates they become genetically, and thus phenotypically, more similar over time compared with groups that do not (Stojanowski and Schillaci 2006). Termed gene flow, or the transfer and movement of alleles from one population to another, this process increases variation at migrant destinations. Communities that do not exchange mates become more dissimilar at a rate determined by the size of the population (Stojanowski and Schillaci 2006). Konigsberg (1990) found that the number of migrants and the distance of migration affected observed phenotypic variance. The isolation by distance framework predicts how, in continuously distributed populations, random mating is limited by distance such that individuals encounter and move to neighboring communities that are closer to them more often than those located farther away, which is in turn reflected in patterns of variance (Wright 1943). If populations follow this

pattern, it is expected that groups nearer to one another will show closer phenotypic similarity. Isolation by distance is closely tied to the idea that localized neighboring gene flow plays the predominant role in shaping regional variation (Hunley 2011). However, interpretations assume populations are evenly positioned over the landscape, and they are exchanging members with their immediately surrounding neighbors for many continuous generations.

2.3.3 Natural Selection and Plasticity

Indicators of natural selection and adaptation are limited when comparing within-group and regional cranial variation on the population level, although evidence suggests populations living in extremely cold environments exhibit facial morphology that deviates from the expected neutral model. Multiple studies have shown that nasal cavity morphology is related to cold and dry climates as they are relative higher and narrower to enhance air turbulence and nasal wall contact compared with those adapted to hot and humid climates (Holton et al. 2013). Climatic variables such as temperature and precipitation are found to influence the maxilla, nasal, and zygomatic height and morphology (Harvati and Weaver 2006; Holton et al. 2010; Roseman 2004). Hubbe et al. (2009) argue that neurocranial morphology is phylogenetically informative, as aspects of face are subject to natural selection, yet this is largely restricted to those living in extremely cold environments in Northeast Asia, North America, and Northern Europe. For example, a study of Buriat, Greenland Inuit, and Peruvian populations shows that they stand out as derived from the neutral model in these comparisons due to extreme climate adaptations (Relethford 2010). Temporal size, but not shape, is found to be reflective of environmental variables including temperature and latitude (Harvati and Weaver 2006; Smith et al. 2007; Von Cramon-Taubadel 2009). The mandible, zygomatics, and maxillae are less aligned with neutral

expectations and significantly reflect diet composition related to subsistence strategy (Smith 2009; Von Cramon-Taubadel 2011).

In an early study of cranial plasticity, Franz Boas published a study entitled *Changes in Bodily Form of Descendants of Migrants* in 1912 that examined the impact of environment on the cranial shape of 13,000 European migrants. Contrasting opinions exist regarding the significance of Boas's migrant study results. Debate is polarized between cranial morphology as mostly heritable versus mostly plastic. Sparks and Jantz (2002, 2003) argue that some of the observations Boas made have statistical credibility, but lack meaning and applicability in terms of modern human variation. Within the debate between cranial morphology as mostly heritable versus mostly plastic, Boas (1912) is generally used to support the latter. Gravlee et al. (2003) come to different conclusions than Sparks and Jantz (2003), although they ask different questions. Gravlee et al. (2003) argue that the t-tests performed by Sparks and Jantz (2003) provide support that migrants and their descendants differ in head form and provide different interpretations both of Boas's questions and hypotheses as well as the results of Sparks and Jantz's (2003) analysis. Relethford (2004) finds that patterns in population structure and organization are not greatly obscured by development plasticity and climate adaptation within the neutral variation model. Others agree that although hominin cranial morphology does show some functional and developmental plasticity, it is not enough to erase biological relatedness reflected in population structure and history (Von Cramon-Taubadel 2009). Therefore, by exploring multi-scalar patterns of within- and between-group morphological similarity, or affiliation, and variation with a population history approach, evidence of migration and gene flow can be elucidated. Representing 3,800 years of agricultural occupation, the Southwest region provides an ideal setting for testing how different migration processes affect human

cranial morphology through time and how such evidence can be applied within the context of cultural affiliation and repatriation.

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FIGURE 1: Map of regional sub-regions in the Southwest

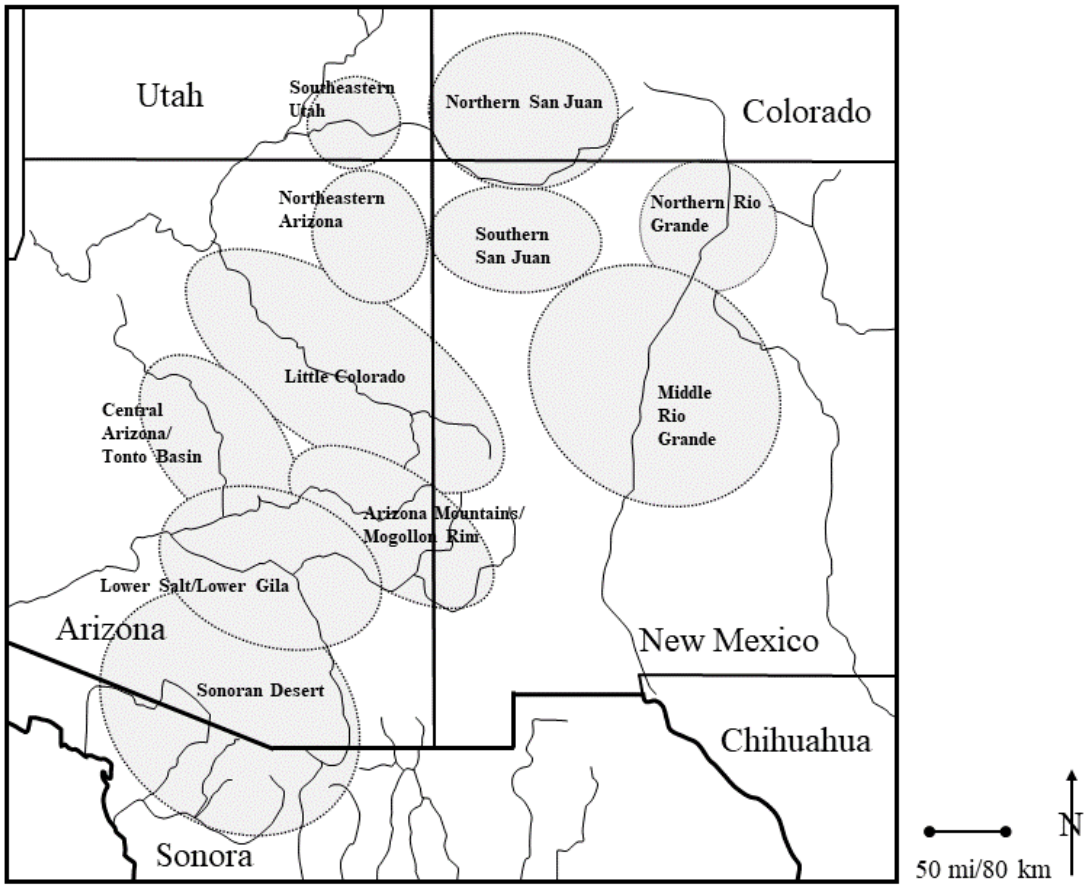

TABLE 1: Composite dissertation samples table

Sub-regions	**Temporal Group**	***n***
Sonoran Desert	2100 BC–AD 50	69
Northern San Juan	500 BC–AD 1275	199
Southeastern Utah	500 BC–AD 1400	128
Northeastern Arizona	500 BC–AD 1400	105
Southern San Juan	AD 920–1275	128
Arizona Mountains/Mogollon Highlands	AD 1200–1400	279
Central Arizona/Tonto Basin	AD 1200–1450	81
Lower Salt/Lower Gila	AD 1150–1450	145
Little Colorado	AD 1100–1700	177
Northern Rio Grande	AD 1250–1600	223
Middle Rio Grande	AD 1325–1700	307
total		1841

APPENDIX A

Biodistance Evidence of Gene Flow from the Kayenta Region

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Abstract

Socioeconomic upheaval and environmental degradation pressured people in the Kayenta region of northeast Arizona to move south into large pueblo communities 800 years ago. This study tests if gene flow followed these migrations. Ten anatomical coordinate points were measured from left temporal bones of 204 individuals from Kayenta Region Black Mesa sites and three large pueblo communities. Results of Canonical Variate, Mahalanobis and Procrustes distances demonstrate significant distances between groups except Point of Pines Pueblo and Black Mesa. This suggests gene flow occurred among Kayenta region immigrants, their descendants at Point of Pines Pueblo, and people from earlier Black Mesa sites representing a pre-migration population. Diverse people buried at Grasshopper Pueblo indicate people of different origins co-resided there, yet gene flow was limited with other groups in this analysis. Migration, co-residence, and admixture that ultimately led to gene flow variably occurred in large pueblo communities south of the Mogollon Rim.

Resumen

Los problemas socioeconómicos y la degradación ambiental presionaron a grupos de la región Kayenta del noreste de Arizona a salir de su territorio hacia al sur formando comunidades mas grandes alrededor de 800 años antes del presente. La evidencia arqueológica sugiere que los migrantes se instalaron en otras comunidades cohabitando con grupos locales. En este estudio se plantea la hipótesis de integración biológica (matrimonio entre grupos) que se suscitó como parte de la integración social. Se tomaron diez medidas cráneo-métricas del hueso temporal izquierdo de una muestra de 204 esqueletos provenientes de sitios en Black Mesa dentro de la región Kayenta y de tres pueblos al centro-este de Arizona (Grasshopper, Point of Pines, y Turkey Creek Pueblos). Los datos fueron analizados en una serie de análisis multivariables incluyendo Variante Canonical, Función Discriminativa, distancia Mahalanobis y pruebas Mantel demostrando que existe una distancia biológica significativa entre todos los grupos con excepción de los sitios de Black Mesa y Point of Pines Pueblo, ya que estos exhiben una afinidad cercana. Posiblemente los inmigrantes Kayenta llegaron a Point of Pines Pueblo por conexiones que existían desde antes de la migración hacia al sur. Los individuos enterrados en Grasshopper Pueblo demuestran una morfología heterogénea indicando una diversidad biológica elevada y menos integración biológica entre los grupos que cohabitaban. Los resultados de este estudio apoyan la idea de que la integración biológica entres los inmigrantes y los grupos locales fue de forma mosaica en lugar de ser en forma más lineal. Las implicaciones metodológicas de este estudio demuestran que el uso del hueso temporal para determinar la afinidad biológica entre grupos prehispánicos puede ayudar a reconstruir las relaciones biológicas e historias poblacionales a través de multiples escalas geográficas y temporales.

This study examines cranial morphological affinity to test if gene flow followed immigration from the Kayenta region into the large aggregated pueblos south of the Mogollon Rim. Social and environmental instability in the Kayenta region of the Colorado Plateau led to rapid depopulation by the end of the thirteenth century. This relocation, referred to as a diaspora, had transformative consequences across the Southwest United States (U.S.) (Clark et al. 2013; Lyons 2003; Mills 2011). Material evidence including perforated ceramic plates, painted pottery associated with the Kayenta region (Maverick Mountain Series) yet produced outside the region, and distinctly shaped kivas provide evidence that people moved into large pueblos located south of the Mogollon Rim in east-central Arizona. Others moved further south to the San Pedro and Safford areas (Dean 1996; Di Peso 1958; Haury 1958; Lindsay 1987; Lyons 2013; Lyons and Lindsay 2006; Mills 1998; Neuzil 2008; Woodson 1999). Not only did this migration affect ceramic technology and architecture, it also affected patterns seen in mortuary practices. Flexed inhumation burials and lambdoidal cranial modification due to cradle boarding infants are bioarchaeological indicators associated with northern Ancestral Puebloan groups, including those from the Kayenta region. Observation of these indicators have helped infer group origin, particularly when found in southern areas where other forms of mortuary practice and cranial modification are more common (Davis 1998; Rodrigues 2008; Whittlesey 1978). It remains unclear from material, mortuary, and previous morphological evidence if the appearance of these indicators was not only synonymous with migration, but also with gene flow between locally originating and migrant groups. To address this possibility, the hypothesis tested is that if the appearance of material evidence associated with the Kayenta region was accompanied by gene flow then less morphological divergence (higher affinity) will be present among immigrants,

their descendants, and Kayenta region individuals representing a pre-migration source population.

Diaspora from Black Mesa

The Kayenta region, located in north eastern Arizona, is characterized by upland mesas partitioned by narrow valleys and canyons, including Marsh Pass, Long House and Laguna Creek valleys, and Tsegi Canyon. Occupation of the region began in the Archaic period and continued through Basketmaker and Puebloan periods (Geib 2011). Maize farmers, who inhabited these localities from A.D. 750 to 900, lived in small dispersed settlements. Habitation sites include well-defined room clusters, masonry rooms for storing and grinding maize, kivas (subterranean ritual structures), and after A.D. 1050, entry boxes in residential rooms (Gumerman 1984; Lindsay and Dean 1983). Such people occupied Black Mesa, located within the Kayenta region of north eastern Arizona from A.D. 800 to 1150. Here seasonal settlement patterns with gradually increasing sedentism and a growing population are evident (Powell 2002; Powell and Smiley 2016). Population size also grew due to an influx of people, expanding marriage networks, and increased fertility from A.D. 950–1150 (Plog and Powell 1984). However, after A.D. 1150 people relocated in short-term migration events representing a diaspora that occurred over 40–50 years (Harrod and Martin 2014; Martin 1991; Martin et al. 2001; Plog 2008).

Drought had become a major obstacle to achieving adequate subsistence in the Kayenta region and forced people to relocate. First, northern Black Mesa was depopulated as people migrated northward to the Kayenta core area or ‘heartland’, and south to ancestral Hopi villages (Dean 1996; Dean et al. 1994; Powell 2002). The Kayenta core area was abandoned around one

hundred years later (beginning A.D. 1250) as the area emptied out from the east to west, and the peak population at Tsegi Canyon left around 1280. Some people moved south into ancestral Hopi villages on the southern fingers of Black Mesa, yet others continued on to large pueblos in east-central Arizona and to the Safford Basin and the San Pedro River Valley during the later thirteenth century (Di Peso 1958; Haury 1958; Dean 1996; Lindsay 1987; Lyons 2003; Stone and Lipe 2011). Archaeological evidence supports this migration was a diaspora as it involved a large number of people moving over a long distance into an already inhabited community (Lyons 2003; Clifford 1994; Mills 2011). People traveled over 300 km from the Kayenta region south, and although material evidence supports their migration and social integration into large pueblos south of the Mogollon Rim, biological evidence is still needed to evaluate and confirm the extent of immigrant and local group interactions.

Moving South of the Mogollon Rim

Diverse people inhabited a landscape of mountains, ridges, canyons, and basins with the Mogollon Rim forming the northern geographic boundary. Lush rivers, creek valleys, and meadows provided fertile land for agriculture. Inhabitants were culturally distinct from other groups living across the Southwest U.S. prior to A.D. 1000 (Haury 1936; Reid and Whittlesey 1995). From A.D. 600–1150 people occupied rectangular pit houses in communities situated along valley floors (Diehl 1997). Great kivas facilitated social integration within and between communities (Gilman and Stone 2013). These communities are located it what is now east-central Arizona and western New Mexico and are sometimes referred to as Mogollon Pueblos (Riggs 2005), with recognized occupation by people from northern pueblo groups in later years (Haury 1985). Increasing birth rates and life expectancy from A.D. 900 to 1200 factored into

population growth in this area as environmental change pushed previously dispersed populations into confined locations with better access to fertile alluvium (Alder et al. 1996; Kohler et al. 2008; Kohler and Reese 2014). Grasshopper, Turkey Creek, and Point of Pines Pueblo represent stages of this transition into large aggregated pueblos that rapidly turned into coalescent communities (Adler 1996; Clark et al. 2013; Reid 1989; Reid et al. 1996).

Grasshopper Pueblo, located approximately 120 kilometers northwest of Turkey Creek and Point of Pines Pueblo, was constructed around A.D. 1275 and expanded by A.D. 1300 as people moved into the community (Reid and Whittlesey 1999; Riggs 2001; 2005; 2013). Two large room blocks are positioned on either side of a perennial stream, and smaller room blocks were constructed around these main architectural units.

To the south, Turkey Creek Pueblo exhibits compact architecture, a series of plazas, a Great kiva, and extramural trash and burial mounds (Lowell 1991; Riggs 2005; Stone 2003). Previous studies report patterns of cranial modification, mortuary accompaniment, and burial flexure frequencies and patterns as evidence for co-residing people who had immigrated from the north into the Turkey Creek community (Davis 1998; Rodrigues 2008). Rodrigues (2008) identified 20 individuals from Turkey Creek Pueblo as Kayenta immigrants based on flexed burial positions and cranial modification type.

Point of Pines Pueblo is located approximately five kilometers south of Turkey Creek Pueblo and has a substantial amount of material and architectural evidence supporting co-residence of Kayenta region immigrants living alongside local people (Haury 1958; Lindsay 1987; Stone and Lipe 2011). Approximately 60–100 people, or 50–60 families, formed the Kayenta immigrant enclave at Point of Pines around A.D. 1265 (Lindsay 1987). A separate contiguous set of rooms was constructed in A.D. 1280–1285 with associated Maverick Mountain

Polychrome ceramics. In addition, a D-shaped kiva positioned 65 meters away is a distinct structural form displaying a different group identity (Dean 1992; Haury 1958; Lindsay 1987; Stone 2003). Lyons et al. (2016) argue that if Kayenta immigrants did not inhabit these rooms they must have resided in another area (or areas) of Point of Pines Pueblo. This implies a higher level of integration between immigrant and local groups than previously thought. Only three people, identified as immigrants by Rodrigues (2008), were not buried in close proximity to local Point of Pines inhabitants which she infers to indicate that co-residence occurred between Kayenta immigrants and local groups.

By A.D. 1300, these rooms and kiva experienced extensive burning, with large quantities of maize, numerous pots, and charred roof beams found associated with the burned structures. Haury (1958; 1989) interprets this as a violent act to drive away Kayenta immigrants. Recent interpretations suggest these rooms had a communal function as a "structure of orientation", rather than being used for residential living, due to their large size, lack of domestic features, and two-story structure (Lyons et al. 2016). A structure of orientation, as defined by Lindsay (1969) and Dean (1996) is a massive architectural unit representing a centralized location in northern settlements from the Kayenta region. Materials found in these rooms more likely reflect ritual disposal of objects and decommissioning of a ritual space (Lyons et al. 2016). After these rooms were burned some Kayenta region immigrants (and their descendants) stayed at Point of Pines for another 150 years and others migrated south to the San Pedro Valley and the Safford Basin, with the presence of Maverick Mountain ceramics indicating their presence after A.D. 1300 at places like Reeve Ruin (Di Peso 1958), the Davis Ranch site (Clark and Lyons 2012), and the Goat Hill site (Stone 2000; Woodson 1999). All three of these large pueblos were largely depopulated by AD 1400, as people migrated north to the Hopi and Zuni regions (Duff 2002).

Previous studies of human morphology, or skeletal shape, suggest continuous biological homogeneity was present in large aggregated pueblo sites in east-central Arizona (Bennett 1973; Shipman 1982). Other researchers report varying trait frequencies and biological distances (biodistances) spanning 200 years (Birkby 1973; Black 1978; Turner 1993). Previous biodistance analyses south of the Mogollon Rim reveal, at minimum, two biologically distinct groups of people resided and were buried within the Grasshopper Pueblo community (Birkby 1973; McClelland 2003). Birkby (1973, 1982) examined biodistance relationships between people buried at Grasshopper, Point of Pines, Kinishba, and Turkey Creek Pueblos, along with intra-site relationships at Grasshopper Pueblo. At Grasshopper Pueblo he found significant distances between biological relationships of people buried on the east and west of the stream that runs through the middle of the site. Based on differences in variation between males and females, he suggests uxorilocal or matrilocal residence patterns. Strontium isotope analyses confirm that adults buried at Grasshopper Pueblo represent both local and immigrant groups (Ezzo and Price 2002; Ezzo et al. 1997; Price et al. 1994). Conversely, Shipman (1982), who also examined these four large pueblo sites, found that people buried here were homogenous. None of these studies include an examination of cranial metrics or testing of hypotheses of migration from Kayenta region populations.

At Point of Pines Pueblo archaeological evidence demonstrates that the Kayenta maintained their own distinct identities (architectural and ceramics), so it is possible that they also maintained distinct biological identities (without gene flow). In order to determine if gene flow occurred among Kayenta region immigrant and local groups at Grasshopper, Turkey Creek, and Point of Pines Pueblos this inter-disciplinary study examines temporal bone morphology from human skeletal remains representing these groups. The hypothesis tested is that if the

appearance of material evidence associated with the Kayenta region was accompanied with gene flow then less morphological divergence (higher affinity) will be present among immigrants, their descendants, and Kayenta regional individuals. By examining the morphological affinity and distance within and between the Grasshopper, Turkey Creek, and Point of Pines Pueblos with the pre-migration Black Mesa group, this study focuses on how immigration from the Kayenta region led to gene flow at these three large aggregated pueblos. It is critical to use biological data and evidence in efforts to understand how migration affected the biology of past populations in the Southwest U.S.

Materials

Well-preserved left temporal bones of 204 people buried at Black Mesa, Grasshopper, Turkey Creek, and Point of Pines Pueblos were chosen for analysis (Figure 1 and Table 1). Both male and female adult individuals (18 + years of age) from Black Mesa sites (Martin et al. 1991:34-37), and from Grasshopper, Point of Pines, and Turkey Creek Pueblos were included. Only those with all 10 landmark coordinates observable were included in analyses (Table 2). Juveniles were excluded as their cranial morphology is not yet fully developed and can skew statistical comparisons of bone shape. Additionally, individuals that had poor temporal preservation or exhibited pathology were also excluded.

Small, yet regionally representative, Kayenta and Mogollon Pueblo population samples are included in this study. Although this study focuses on the variation and affinity among a limited number of people assumed to represent those living during this time in both regions, bioarchaeological studies in the Southwest U.S. need to incorporate available morphological

evidence to help understand how people were related and organized in the past. By standardizing and pooling male and female samples, site group sample sizes are maximized.

Previous studies use cranial modification, mortuary practices, and strontium isotopes to distinguish immigrants and locals. Rodrigues (2008) utilized cranial modification type and mortuary practices to identify immigrants at Point of Pines and Turkey Creek Pueblos. She identified two adult females included in this study (Burials 83 and 187) buried at Point of Pines Pueblo as immigrants from the Kayenta region based on the presence of lambdoidal cranial modification, yet they were buried in the supine position (on their back) characteristic of mortuary practices observed south of the Mogollon Rim (Reid 1989). Rodrigues (2006:385) also identified three individuals as immigrants buried at Turkey Creek Pueblo that were included in this study; two adult males (Burial 90 and 92) and one adult female (Burial 209). Burial 90 was found semi-flexed, Burial 209 was flexed, and Burial 92 had lambdoidal cranial modification (Rodrigues 2008: 381-382).

Twenty-two individuals from Grasshopper Pueblo included in this analysis (seven males and 15 females) were identified as immigrants based on strontium isotope data (Ezzo et al. 1997: 452–453). Initial statistical analyses were conducted on all individuals, and secondary analyses conducted excluded identified migrants from Turkey Creek, Point of Pines, and Grasshopper Pueblos to examine changes in biological distance and affinity while controlling for immigrant phenotypes.

Methods

Morphology and migration

Human skeletal morphology has been used to track genetic relationships among prehistoric groups by researchers in the Southwest U.S. since the late ninetieth century, although theoretical frameworks and methods have developed considerably since this time (Buikstra et al. 1990; Corrucini 1972; 1998; El-Najjar 1978; Mackey 1977; O'Donnell and Ragsdale 2017; Ortman 2012; Schillaci 2003; Schillaci and Stojanowski 2003; Stojanowski and Schillaci 2006). Human cranial morphology is now widely agreed to proportionately reflect genetic relationships due to moderate heritability, allowing it to be used as a proxy for reconstructing population structure and ancestral origins (Carson 2006; Hugo-Centeno et al. 2016; Martinez-Abadiás et al. 2006; 2009).

Recent studies look at how time and geographical factors explain aspects of population affinity such as the effects of gene flow and drift (Keita and Boyce 2008; Nikita et al. 2012; Relethford 1996; Sutter and Verano 2007). Migration leads to closer biological distances and affinity between groups experiencing gene flow, and higher within-group variation (Relethford 2004; Roseman 2004; Steadman 2001). If the presence of materials, architecture, and bioarchaeological patterns associated with people from the Kayenta region support that migrant and local groups became more integrated overtime and involved gene flow, it is expected that less morphological divergence and higher affinity will be observed.

Temporal bone morphology has received considerable attention recently as a neutral genetic indicator to test phylogenetic and population history hypotheses. The constrained development of the temporal bones closely follows the shape of the brain and inner ear as the left and right flat portions provide a transition between the vault and base and are formed

intramembranously. (Harvati and Weaver 2006; Lockwood et al. 2002, 2004; Smith 2009; Smith et al. 2007, 2013; Terhune et al. 2013; von Cramon-Taubadel 2009). The petrous portion that houses the inner ear forms endochondrally, or with a cartilaginous precursor (Scheuer and Black 2004; Lieberman 2000; 2013). Many researchers argue that due to the developmental nature of the temporal bone, it has morphology that closely coincides with neutral genetic distances not affected as intensively by selection (Harvati and Weaver 2006; Smith et al. 2007; Smith 2009; Von Cramon-Taubadel 2009).

The robusticity of temporal bones compared with cranial vault and face elements allows them to resist taphonomic destruction that is often pervasive in prehistoric skeletal remains (White and Folkens 2005). Cradle boarding primarily affects the shape of the occipital and sometimes posterior parietal vault bones by applying direct localized pressure, and is widely, yet variably, observed in Southwest U.S. populations (Hrdlička 1935; Kohn et al. 1995; Stewart 1937). Kohn et al. (1995) used Finite Element Analysis to demonstrate that the effects of lambdoidal flattening were minimal on the cranial base (including the temporal) and face of ancestral Hopi individuals from the site of Wàlpi (Qöötsaptuvela). Parietal and occipital measurements altered by cradle boarding were not included in this study as most individuals in the sample exhibit artificial cranial modification. Most maxillae (lower face bones) exhibited substantial tooth loss with bone remodeling and thus were also not included.

Temporal shape was quantified using ten coordinate points from adult left temporal bones with a Microscribe 3DX digitizer (Figure 2, Table 2). The digitizer is an efficient way to collect geometric morphometric data (Hildebolt and Vannier 1988; Ousley and McKeown 2001). Each temporal measured was positioned on three stable, hand-made clay pillars to allow for coordinate point data collection from all angles while keeping the bone from moving. Coordinate landmark

or anatomical loci were recorded by the author from each well-preserved left temporal bone focusing primary on the petrous portion that houses the inner ear, location and dimensions of arteries and nerve openings, and external auditory meatus dimensions (external opening of the ear).

Data Processing and Measurement Error

Data processing and analyses were conducted in MorphoJ (Klingenberg 2011). Generalized Procrustes Analysis (GPA) was first used to rotate, translate, and scale landmark coordinates to remove size differences (Badawi-Fayad and Cabanis 2007; Mitteroecker and Bookstein 2009; Rohlf and Slice 1999). This process systematically places temporal bones on a common scale, fits geometric centers, and minimizes gaps between anatomical landmark points (Rohlf 1990). Overall, the process of GPA reduces effects of size, position, and orientation allowing for unbiased male and female crania to be pooled in order to maximize sample size. To assess measurement error, the set of ten temporal landmarks were collected twice from eight randomly chosen individuals on separate occasions. These coordinates were subjected to GPA, and the largest Procrustes distance was compared with the smallest distance in the Kayenta, Grasshopper, Turkey Creek and Point of Pines groups in order to assess whether configuration precision was less than intra-sample variation (Bastir et al. 2008; Nikita 2012; Terhune et al. 2007).

Seven outliers were identified using MorphoJ, including one each from Turkey Creek, Point of Pines, and Black Mesa along with four from Grasshopper Pueblo. None of these outliers were identified as immigrants in previous studies, and they moderately skewed observed affinity patterns possibly due to origins outside of the Southwest U.S., developmental or pathological

experiences, or measurement error. Although important to recognize, these outliers were removed in order to eliminate their effects on morphological affinity patterns.

Assumptions and Limitations

Temporal morphology represents only a glimpse of the variation present in past populations. Using geometric morphometrics to assess distance and affinity assumes temporal shape similarity has a genetically heritable basis. As with many bioarchaeological studies, preservation often constrains available sample sizes. Dividing individuals into smaller groups based on tighter chronological phases or periods to assess changes in affinity overtime was not feasible due to these sample size limitations. The temporal bone encompasses and stabilizes the temporo-mandibular joint (TMJ) when chewing which introduces forces inducing bone remodeling and variability according to toughness of diet. The mastoid process, which serves the insertion location for the sternocleidomastoid muscle, was not included in the shape analysis of the temporal bone due to its variability and sexual dimorphic characteristics. Although human cranial morphology does show some functional and developmental plasticity, it is not enough to erase similarity due to biological relatedness (Collard and Wood 2007; Relethford 2004; on Cramon-Taubadel 2009).

Significant developmental instability and disease likely did not substantially affect cranial morphology in this study (East 2008; Martin et al. 1991). In a study of juvenile health based on human remains from Grasshopper, Point of Pines, and Turkey Creek Pueblos, all three sites showed similar frequencies of antenatal and postnatal pathology, with evidence that children lived with mild to moderate chronic nutritional stress, yet maintained relatively good viability (East 2008:276). Similar findings were also present among Black Mesa individuals, particularly

in the later period (A.D. 1050-1150) when instances of dental hypoplasia increased (Martin et al. 1991). Although these limitations are present, temporal morphology provides a new valuable insight on reconstructing relatedness in past human populations.

Analysis

Covariance and Principal Components Analysis (PCA)

Covariance matrices are calculated first on derived Procrustes coordinates for the combined sample, and again on the total sample minus previously identified immigrants. The initial goal in conducting shape comparisons using multivariate analyses involves reducing a set of variables to summarize the variance present in order to address mean shape and covariance (Slice 2007). Covariance matrices are then subjected to Principal Components Analysis (PCA) to reduce dimensionality of shape variance present by identifying the linear combination of maximum variance in order to summarize it and help visualize how groups are related (Lawing and Polly 2010; Rechner 1992; Slice 2007). These initial ordination steps allow for further multivariate analyses using Procrustes coordinates.

Canonical Variates Analysis (CVA)

Canonical Variates Analysis is conducted twice in SPSS 24 (IBM) to determine the maximum difference between Grasshopper, Point of Pines, and Turkey Creek Pueblo and Black Mesa groups, first including all individuals and again after excluding previously identified immigrants (Figure 3). Canonical variates are linear functions associated with canonical correlations between sets of variables (Rencher 1992). By maximizing group differentiation through ordination, CVA works to classify two or more groups designated *a priori*, along axes

that best represent variation (Cooke and Terhune 2015; Lawling and Polly 2010). Some argue that CVA is not as useful in geometric morphometric analyses because dimensionality is greatly reduced (see Mitteroecker and Gunz 2009). However, CVA scatterplot results aids in interpretation of affinity and relatedness by plotting each individual included in the analysis in relation to one another, and helps visualize how site groups overall are related. Mahalanobis distances (d^2) and Procrustes distances are also generated using CVA and MorphoJ, and significance in pairwise distances tested through permutation (x10000).

Geographic Distance and Mantel Tests

Since matrices violate statistical assumptions of traditional correlation tests, a Mantel test is used to calculate correlation between Mahalanobis distances and geographic distances (Table 3) between each sample (Mantel 1967). The main purpose of incorporating a Mantel test is to also consider if patterns in affinity and biological distances between defined groups are attributed to geographic distance, following an isolation by distance model (McKeown and Jantz 2005; Wright 1943). PASSaGE software is used to calculate the Mantel test between these matrices, and significance was tested with permutation (x10000).

Results

To assess measurement error, left temporal bones from eight individuals (two from each site sample) were measured twice and subjected to GPA individually. The range of Procrustes distance values obtained from individuals measured twice was d = 0.018– 0.051. Following Bastir et al. (2006) and Nikita et al. (2012) coordinate measurement variation between

individuals measured twice is much less than inter-group variation indicating intra-observer error is minimal.

The results of the CVA (Figure 3) demonstrate dissimilarity between Grasshopper Pueblo compared with the two other pueblos and Black Mesa groups on the x-axis representing Canonical Variate 1 (55–57% of total variance). Most people from Grasshopper Pueblo do not show affinity with other site groups on the x-axis. This indicates that Grasshopper has a relatively different within- and between-group affinity pattern compared with Black Mesa, Turkey Creek, and Point of Pines Pueblos. Turkey Creek Pueblo and Black Mesa diverge mostly on the y-axis representing Canonical Variate 2 (32–33% of total variance). In the CVA including migrants, the Black Mesa sample and Point of Pines Pueblo have the closest canonical variate group mean as indicated by confidence ellipses with a probability set at 95%. When migrants are excluded, and the CVA is re-calculated the relationship between the Point of Pines Pueblo and the Black Mesa sample becomes only slightly more distant as represented in the left scatterplot in Figure 2. Overall, affinity patterns show little change when comparing CVA scatterplots including and excluding identified migrants.

Mahalanobis distances (Table 4 and Table 5) were converted to squared distances and sample size bias was corrected following Marcus (1993). All Mahalanobis distances between site groups were significant at the 99% confidence level indicating each group is relatively morphologically distinct. When immigrants are included in the analysis (Table 3), the largest Mahalanobis distance is present between Turkey Creek Pueblo and the Black Mesa groups ($d^2 =$ 3.798). The smallest distance present is between the Black Mesa and Point of Pines Pueblo groups ($d^2 = 1.437$). Procrustes distance results (Table 4) show the greatest distance between Grasshopper and Black Mesa ($d^2 = 0.098$), and the distance between Point of Pines Pueblo and

Black Mesa sample ($d^2 = 0.051$), is the only distance not significantly different. Mahalanobis and Procrustes distance matrices encompassing all four groups were tested for correlation against a geographic distance matrix (Table 3) using a Mantel test. Distances presented in Table 5 exclude identified immigrants, yet follow the same biodistance affinity patterns.

Procrustes distances result show the greatest distance between Grasshopper and Point of Pines Pueblo, and the distance between Point of Pines Pueblo and Black Mesa sample is the only distance not significantly different. Mahalanobis and Procrustes distance matrices encompassing all four groups were tested for correlation against a geographic distance matrix using a Mantel test. Results find that geographic distance matrices are not significantly correlated at the 95% confidence level with Mahalanobis (r = 0.3812; p = 0.653) and Procrustes (r = 0.4018; p = 0.287) distances. These results demonstrate that the isolation by distance model does not explain the patterns of affinity between Black Mesa, Point of Pines, Turkey Creek, and Grasshopper Pueblo groups, and geographic distance is not considered a major factor influencing affinity between site groups.

High affinity between those buried at Black Mesa sites and people buried in Point of Pines Pueblo is resented in the CVA scatterplot, and Mahalanobis and Procrustes distance analyses. If this affinity is attributed to gene flow occurring between Kayenta region immigrants and locals at Point of Pines Pueblo, these results parallel archaeological inferences of intermarriage and admixture following co-residence. Although removing previously identified immigrants from the analysis shifted patterns slightly, Black Mesa and Point of Pines Pueblo biological distances were not substantially affected. Results also reveal relatively high morphological diversity present at Grasshopper Pueblo possibly attributed to immigrants from regions not included in this study.

Discussion

Higher affinity observed between people buried at Black Mesa and Point of Pines indicate gene flow likely occurred between these co-residing groups. Results show that when immigrant individuals are included in the analysis, Point of Pines and Black Mesa individuals show closer affinity then when immigrants are excluded from the analysis. Although as a group Grasshopper is distant (Figure 3, Tables 3 and 4), some individuals do overlap with the other groups in the study. This indicates that some Grasshopper inhabitants were in fact closely related to a sub-set of people buried at the other site groups. One important feature of migration during this time involves the fluidity, flexibility, and transformative impact it had on social and biological boundaries as immigrants interacted with local populations which in turn spurred change across the Southwest US (Clark et al. 2013; Stone 2003). One example involves the distinctive ceramic tradition, referred to as the Salado phenomenon, which spread across the southern Southwest reflecting social transformation (Clark 2001; Clark et al. 2013; Crown 1994; Dean 2000; Lyons 2003). So although these distinctive aspects of material culture and technology associated with the Kayenta region persisted south of the Mogollon Rim, gene flow was not constrained after migration in communities like Point of Pines, yet was likely more limited between Turkey Creek, Point of Pines, and Black Mesa and communities such as Grasshopper Pueblo.

Dynamic social networks led to increasingly heterogeneous societies south of the Mogollon Rim during the thirteenth and fourteenth centuries (Cameron and Nelson 2011). Morphological affinity appears to be much more diverse at sites where multi-regional immigrants and local people co-resided such as at Grasshopper Pueblo. More than one third of people living at Grasshopper Pueblo were identified as immigrants through isotopic analysis, yet

only a portion of those living at Grasshopper migrated from the north (Ezzo et al. 2002). This explains the large biological distance between Grasshopper Pueblo and the Black Mesa individuals. Lowell (2007) argues that conflict and warfare pushed women refugees into the Grasshopper area, resulting in more females than males inhabiting the site; which is reflected in unequal burial distributions. Alternatively, CVA results do not control for differences in sample sizes which may also play a role in Grasshopper Pueblo's morphological affinity distribution. Long-distance connections, with some exceeding 250 kilometers, were critical to survival during times of depopulation, migration, and coalescence. For example, strong ties during drought periods were important for managing potentially severe crises in many areas of the Southwest U.S. (Borck et al. 2015; Mills et al. 2013). Results presented here indirectly support that biological networks likely helped maintain connections initialized via migration and co-residence. Interactions that follow migration are an essential component influencing morphological changes and population structure (Fix 1999; Guillaume 2011; Wells and Stock 2011). Stodder (2006) argues that across the pre-contact Southwest U.S. intermarriage and admixture helped build and maintain social and economic networks, defense alliances, community cooperation, and solidarity among and between site inhabitants.

Migration provides a cultural and biological context for microevolutionary mechanisms (gene flow, genetic drift), in that migratory success depends on reproductive success (Wells and Stock 2007). "Push-pull" factors are often considered in archaeological studies of migration. Changes in social and economic circumstances are broken down into pushes from one settlement and pulls to a pre-determined destination (Anthony 1990). Environmental and economic pushes, such as drought, resource over-exploitation, and population pressure in addition to socio-political factors can drive people to migrate. Environmental pulls were also an important influence in the

Southwest U.S. driving people to find and follow perennial water and fertile agricultural land (Clark 2001; Herr and Clark 1997). An additional migration pull factor not often considered in archaeology is the opportunity for establishing biological ties and networks (Campbell and Barone 2012). Thus, small-scale admixture resulting from migration and subsequent co-residence in prehistoric communities was an initial benefit as it increased diversity, social buffering, and viability of all groups involved. As people moved from the Kayenta region, gene flow with groups in established communities likely followed co-residence and admixture that was critical to both social and biological survival into future generations.

Fix (2012) argues that migration and dispersal have the same general costs and benefits among humans as other species except that our decisions are more complicated and involve kinship rules and relationships. Kin-structured migration, involving people who move to locations due to the presence of related kin groups, are attracted to these locations over others due to pre-existing connections and ensured cooperation (Campbell and Barone 2012). In small-scale societies this is particularly important as kinship is often the foundation of social organization. Kin structured migration into established communities also increases within-group variation initially before intermarriage and gene flow occurs (Fix 1978; 2004; Neel and Salzano 1967: Rogers 1987).

Biodistance analysis has the ability to clarify and confirm archaeological reconstructions of human movement and migration (Howell and Kintigh 1996). Migration of people from the Kayenta region south provided the catalyst for cultural and biological integration in the Southwest U.S. The results of this study support interpretations of co-residence made from archaeological evidence, and provides bioarchaeological evidence that gene flow occurred between immigrant and local groups, although to variable extents. Migration, co-residence,

intermarriage, and admixture built community solidarity that resulted in gene flow south of the Mogollon Rim, which ultimately impacted the survival of multiple diverse groups across the Southwest U.S. region.

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Figure 1: Map showing locations of site groups included in this study

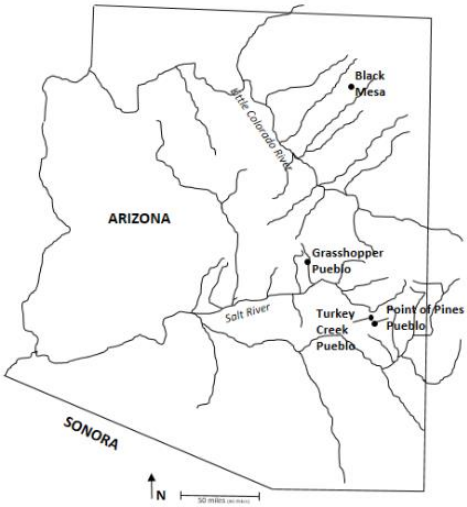

Figure 2: Diagram of left temporal bone and position of landmark coordinate points collected

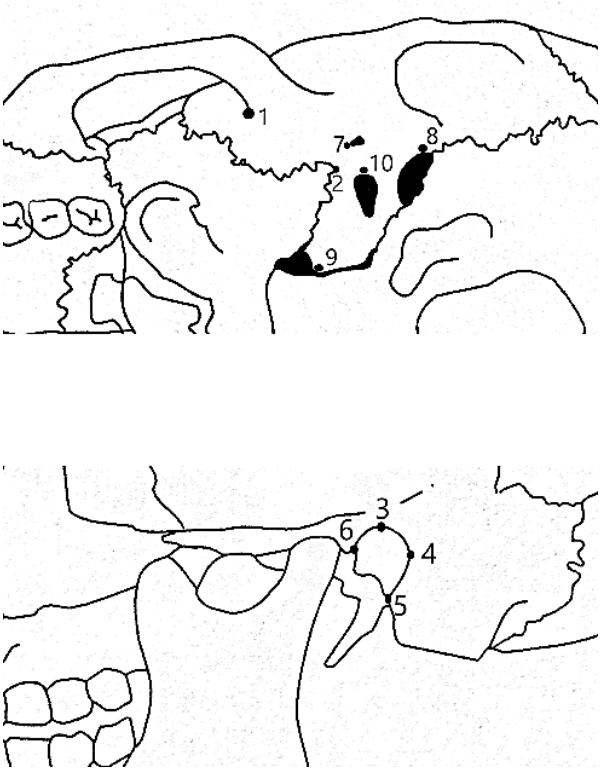

Figure 3: Canonical Variates Analysis (CVA) including immigrants (left, A) and excluding immigrants (right, B) with confidence interval ellipses highlighting the position of site group centroids

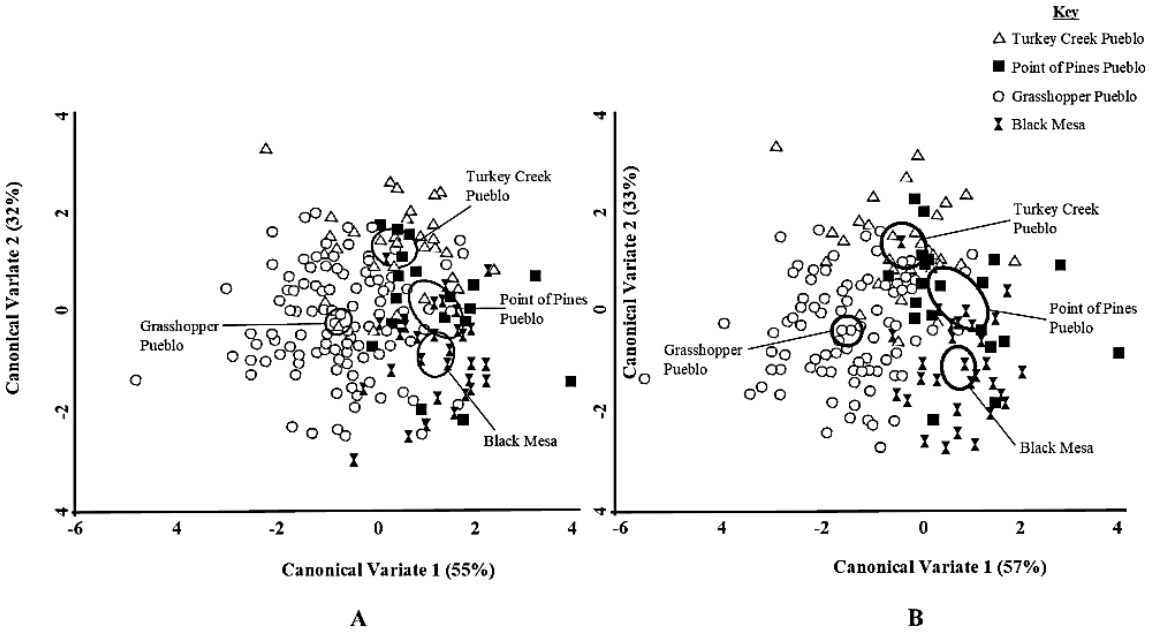

Table 1: Site group samples included in this study

Site groups	Date Range	Males	Females	*n*
Black Mesa	A.D. 800–1150	14	17	31
Turkey Creek Pueblo	A.D. 1240-1300	18	17	35
Point of Pines Pueblo	A.D. 1250–1400	10	15	25
Grasshopper Pueblo	A.D. 1275–1400	42	71	113
Totals		**84**	**120**	**204**

Table 2: Description of temporal bone coordinate landmark points collected

ID	Landmark	Anatomical Definition	Source
1	Temporal fossa (posterior)	Most posterior, inferior point on the temporal fossa	1
2	Stenion	Most medial point on the sphenosquamosal sutures	2
3	Porion	Most superior point on the margin of the external auditory meatus	2
4	Ext auditory meatus (posterior	Most posterior point on the margins of the external auditory meatus	1
5	Ext auditory meatus (inferior)	Most inferior point on the margins of the external auditory meatus	1
6	Ext auditory meatus (anterior)	Most anterior point on the margins of the external auditory meatus	1
7	Styloid foramen	Most anterior, inferior point on the styloid foramen	3
8	Juglar (lateral)	Most inferior, lateral point on the margin of the jugular foramen	4
9	Petrosal	Most anterior point of the petrous element on the temporal bone	4
10	Carotid canal (lateral)	Most lateral point on the carotid canal	3

1. Lahr (1992); 2. Martin and Sailer (1957); 3. von Cramon-Taubadel (2009); 4. Lockwood et al. (2004)

Table 3: Unbiased Mahalanobis (d^2) (top half) and Procrustes (bottom half) distance matrices, including immigrants

	Black Mesa	Turkey Creek	Point of Pines	Grasshopper
Black Mesa	0.000	3.798***	**1.437****	3.739***
Turkey Creek	0.092***	0.000	2.506***	2.831***
Point of Pines	**0.051**	0.065**	0.000	3.659***
Grasshopper	0.098***	0.058**	0.082***	0.000
*	$p \leq 0.050$			
**	$p \leq 0.010$			
***	$p \leq 0.001$			

Table 4: Unbiased Mahalanobis (d^2) (top half) and Procrustes (bottom half) distance matrices, excluding immigrants

	Black Mesa	**Turkey Creek**	**Point of Pines**	**Grasshopper**
Black Mesa	0.000	5.029***	2.329***	4.728***
Turkey Creek	0.096***	0.000	2.583***	3.394***
Point of Pines	**0.055**	0.069***	0.000	4.792***
Grasshopper	0.110***	0.065***	0.097**	0.000
*	$p \leq 0.05$			
**	$p \leq 0.01$			
***	$p \leq 0.001$			

Table 5: Geographic distance matrix (miles/kilometers)

	Black Mesa	Turkey Creek	Point of Pines
Turkey Creek	187 mi/300 km		
Point of Pines	190 mi/305 km	3 mi/5 km	
Grasshopper	140 mi/225 km	75 mi/120 km	78 mi/125 km

APPENDIX B

Reconstructing Population Histories Using Biological Distance in the North American Southwest (2100 BC–AD 1700)

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Abstract

Diversity among contemporary Native peoples of the North American Southwest is a consequence of complex population histories involving repeated and overlapping migrations. This study tests four migration processes: [1) colonization of open landscapes, 2) internal frontiers, 3) diaspora, and 4) coalescence and reorganization], to reconstruct how migration impacts biological relatedness through time. Following the Relethford-Blangero analytic model, phenotypic variation and biological distances are calculated based on craniofacial measurements collected from 1,299 individuals spanning 3,800 years of occupation in the Southwest. Two early ancestral lineages emerged in the northern Southwest, and there is evidence of migration from the Sonoran Desert to the San Juan River drainage and Northeastern Arizona. Settlement density pushed people into internal frontiers, which led to genetic drift through founder's effect and localized admixture. Long-distance diaspora contributed to heightened diversity at both origin and destination sub-regions, such as in Northeastern Arizona and the Arizona Mountains. Close biodistances between the western Zuni River (late) and eastern Galisteo Basin sub-regions provide support that migration traversed region during times of reorganization. This study demonstrates how cranial morphometrics has implications for diachronically tracking migration processes within a population history framework.

Migration plays an enduring role in shaping human population trajectories, yet archaeological and biological lines of evidence used to understand past migration are often approached separately. Archaeologists have long been interested in identifying and tracing migrations through the material record; however, Cameron (1995) suggests that inadequate definitions of what constitutes migration severely limit its utility in reconstructing archaeological scenarios. Clark and colleagues (2013:400) define migration in non-complex societies as "long-term residential relocation by one or more discrete social groups across community boundaries in response to spatially uneven changes in social and economic conditions". In the North American Southwest, oral traditions of Native peoples include migration stories that originate from distinct locations, pass through numerous transitional sites, and are linked to group identity (Bernardini 2008; Bernardini and Fowles 2011; Duff 2002; Ferguson 2007). Ortman and Cameron (2011) caution that social context must be considered on a case by case basis when inferring migration from material incongruities representing past populations. They propose that causes, size, nature and pace, and how migrants integrated within established communities at destination locations are dimensions of social context to consider when developing migration theory.

Exploring biological relationships between past communities can provide critical insights into the consequences of migration. Previous studies of North American Southwest cranial morphology document generalized continuity influencing widespread biological relatedness across the region (Corruncini 1972; El-Najjar 1978; Shipman 1982) that originated from several distinct founding lineages (LeBlanc et al. 2007; 2008; Ortman 2012). As new explanatory models, statistical methods, and data are developed and become available, a re-examination of long-held assumptions about biological continuity and gene flow associated with archaeological models of migration is necessary. Biodistance studies conducted outside of the Southwest

indicate that geographic, temporal, and cultural barriers can potentially affect population histories by limiting gene flow through time (Keita and Boye 2008; Nikita et al. 2012; Ross et al. 2008; Steadman 2001). Therefore, it is imperative to integrate biological and material evidence of migration with a population history approach.

The goal of this study is to test biological expectations of four migration processes within three temporal periods across the Southwest by applying a population history and biological distance (biodistance) approach. Here, I examine how archaeologically inferred migration processes of colonization of open landscapes, aggregation and movement into internal frontiers, diaspora, and reorganization differentially directed processes of gene flow and genetic drift diachronically. In addition, I revisit the measurement of cranial morphology as a biologically valid and accessible technique to help understand the impacts of migration. This technique is applied in order to reconstruct population histories by integrating archaeological and biological evidence.

Processes of migration are integral to understanding human social and biological relationships and organization throughout the Southwest. This study tests biological expectations following four migration processes: [1) colonization of open landscapes, 2) migration into internal frontiers, 3) long distance diaspora, and 4) coalescence and reorganization)] across three temporal periods, the Early period (2100 BC–AD 500), Middle period (AD 700–1400) and Late period (AD 1100–1696) (Table 1). I concentrate on 28 geographically and temporally defined sub-regions to test how migration impacted phenotypic variance and biological affinity over 3,800 years of occupation. These sub-regions are represented by bounded areas due to the necessity of creating comparative discrete groups (Figure 1). Sub-regions are defined primarily by geographic features including river drainage and tributary systems, mountainous and desert

areas, valleys, and basins. In addition, sub-region boundaries are representative of the crania included in this study. Three time periods are used to categorize the sub-regions, including the Early (2100 BC–AD 500), Middle (AD 700–1400), and Late (AD 1300–1700) periods. Additionally, it is important to highlight that not all sub-regions are considered due to lack of accessibility and preservation of human skeletal remains at the time of data collection and analysis.

Migration research can be divided into four categories including detection, motivation, organization, and impact (Clark 2001; Herr and Clark 1997). Early archaeologists focused on pottery and architectural style to identify evidence for migration throughout the northern Southwest, often linking modern Puebloan peoples to past ancestral sites (Fewkes 1904; Haury 1958; Kidder 1924). Based on his work at Point of Pines Pueblo, Haury (1958) identified material signatures indicative of migration such as the sudden appearance of non-local traits, hybridization of cultural traits, and chronological correlation between origin and destination sites (Cordell 1995). Material approaches in migration research often focus on frequency and variability in technological style expressed in ceramics, architecture, and mortuary practices (Carr 1995; Clark 2001; Eckert 2008; Lyons 2003; Neuzil 2008; Spielmann 1998). In particular, low visibility material indicators of enculturation are focused on to reveal learned ceramic manufacturing behaviors connected with specific cultural areas (Carr 1995; Clark 2001).

Push-pull factors motivating migrations include environmental change contributing to drought and famine, social upheaval, conflict, and economic pressures (Anthony 1990; LeBlanc 1999; Lowell 2007). Exchange networks, marriage pools, and esoteric knowledge can also influence migration histories (Eckert 2008). Recently, questions have shifted from a focus on migrant-host connections to migration as coerced, unplanned or due to conflict against the

logistical backdrop of duration, pace, group size and the composition of migrating groups (Cameron 2013; Mills 2011; Ortman and Cameron 2011). For example, Mills and colleagues (2016) demonstrate that long-distance migrations often occurred in point-to-point leaps across the landscape, rather than occurring in waves, indicating far-reaching social networks. Furthermore, evolutionary mechanisms stemming from migratory behavior, including genetic drift, gene flow, and selection, depend on the reproductory success of migrant groups (Wells and Stock 2012). These biological factors are primarily addressed as diachronic impact of migration on, in this case, Southwest sub-regional population histories. This study considers whether different forms of migration have measurable biological consequences, which in turn have major implications for the reconstruction of past population histories. The following sections introduce and propose four processes of migration based upon archaeological inferences that are in turn tested with corresponding cranial morphometric data.

Colonizing Open Landscapes

Migration into, and colonization of, open landscapes describes the movement and settlement of small-scale forager-farmers into relatively unoccupied locales due to relatively favorable conditions and availability of resources. This type of migration occurs when highly mobile groups seek fertile land and ample resources in rapid migrations that cover wide expanses of territory (Barton et al. 2004; Goebel et al. 2008). Colonization is used here to mean the establishment of a new home range by a social group (Ortman and Cameron 2011).

Initial migrants move into an open landscape carrying only a subset of the biological and cultural variation present in their natal homeland (Bellwood 2013). This variation becomes magnified as the populations grow and become differentiated from the homeland population overtime. This form of migration lays the foundation for an increased number of long-term settlements, and

thus, successive point-to-point migrations from one settlement to another. The colonization into open landscapes describes the earliest migrations into the North American Southwest as small forager groups rapidly moved across large territories in the region.

Around 5,000 years ago, lower temperatures and increased precipitation attracted hunter-gatherers to the Sonoran Desert and allowed access to fertile floodplains. These environmental conditions aided in the gradual transformation from hunter/gatherer to forager/farmer as material evidence suggests extended use localities following seasonal patterns of peak resource availability (Huckell 1996; Mabry 2005). A significant decrease in residential mobility is reflected in material culture patterns with similar artifact types found throughout the Southwest region (Diehl 1997; Gregory 2001; Mabry 1997; Sliva 2015). McBrinn (2005) reports projectile point styles associated with Late Archaic Mogollon caves that she attributes to regional social networks that provided information on subsistence resources. This suggests groups at all contemporaneous site complexes either shared the same culture or had abundant social interaction (Mabry 2008).

People who lived during the Early Agricultural period (2100 BC–AD 50) in the Sonoran Desert of southern Arizona as inhabitants of some of the earliest long-term residential settlements associated with agricultural investment (Byrd 2014; Carpenter et al. 2005; Huckell 1995, 1996; Mabry 2008; Roth and Freeman 2008; Vint 2017). By 1500 BC, maize is found throughout the North American Southwest, yet substantial investment in farming begins in the Sonoran Desert with the construction of the earliest irrigation canals north of central Mexico (Vint 2017). Debates surrounding the origins of these early farmers are tied to inferences that they migrated north from central Mexico (Berry and Berry 1986; Haury 1962), and that they were members of the Proto-Uto-Aztecan language community (Bellwood 2001; Hill 2001).

Others argue that cultigens spread by diffusion across diverse groups into the region and were subsequently locally adopted (Matson 1991; Merrill et al. 2009; Roth 1996; Wills 1990, 1995).

Evidence for the earliest farmers on the Colorado Plateau, located in the northern Southwest, is associated with early groups living within the San Juan River drainage system who are referred to as Eastern (Northern San Juan) and Western (Western San Juan, Northeastern Arizona) Basketmaker II following the Pecos classification system (Charles and Cole 2006; Lipe et al. 1999). Archaeologists have long recognized the material differences between these early groups which are suggestive of separate origins and population histories (Matson 1991; Morris and Burgh 1954). Groups in the eastern portion of the northern San Juan River drainage (Eastern Basketmaker II) are interpreted as descendants of local Great Basin-Colorado Plateau Archaic populations with prolonged *in-situ* development (Charles 2000; Matson 1991). Conversely, Western Basketmaker II groups living in the western portion of the San Juan River drainage and Northeastern Arizona share several material similarities, including projectile point style, with groups from the Sonoran Desert, which has led to inferences regarding northward migrations from the Sonoran Desert between 850 and 500 BC (Berry and Berry 1986; Geib 2011; Matson 1991; Sliva 2015). These two migration scenarios, migration from the Sonoran Desert north to Western San Juan and Northeastern Arizona, and discrete population histories between Early groups living along the San Juan are proposed as two long distance migration processes that occurred as people first colonized uninhabited landscapes in the region.

Sites in four sub-regions, the Sonoran Desert, Western San Juan, Northeastern Arizona, and Northern San Juan, were inhabited during the Early period (2100 BC–AD 500) as they represent the earliest agricultural occupations in the region. Figure 2 illustrates the archaeologically inferred migration of early forager farmers from the Sonoran Desert sub-region

north to the Northeastern Arizona (early) and Western San Juan sub-regions. If long-distance migration and gene flow occurred into open landscapes from the Sonoran Desert north to the Western San Juan and Northeastern Arizona, then close biological affiliation between these sub-regions following archaeological inferences is expected. If this archaeological model is accurate, then Sonoran Desert, Northeastern Arizona (early), and Western San Juan sub-region samples will show close biological distances and significantly high variance, with the Northern San Juan (early) sub-region being relative distinct, indicating separate population histories. Although hypothesized to be from different origins, it is possible that Western San Juan, Northeastern Arizona, and Northern San Juan sub-regions experienced gene flow due to their close geographic proximity which may obscure expected patterns inferred from long distance migration from the south.

Migration into internal frontiers

Migration into internal frontiers and long distance diaspora are tested within the Middle Period (Figure 3). The aggregation of large villages and migration of people into internal frontiers are processes that are closely connected. Over time as agricultural communities become denser and resources more constrained, people disperse into more sparsely occupied areas called internal frontiers (Herr 2001; Kopytoff 1987). Through his research on African tribal societies, Kopytoff (1987) found that populations moved into frontier areas located between aggregated settlements. Famine, conflict, and witchcraft accusations were identified as pushing kin-based groups away from larger settlements. Ogundiran (2014) argues that internal frontiers are diverse, interstitial spaces that can serve as buffer zones between aggregated communities, zones of expansion, and as crossroads of trading and political networks. It addition, they serve as cultural boundaries of ethnolinguistic groups. The availability of fertile land and economic opportunities

can act as pull factors in decisions to migrate into internal frontiers if resources are limited in more aggregated communities and more densely populated areas.

Diaspora

Diaspora is a type of migration that can occur as the result of crises and upheaval that motivates people to move and resettle a long distance away in already occupied locales (Clifford 1994; Cohen 1997). Lateral connections are generally maintained among diasporic communities (Clifford 1994). Diasporic migrations comprise of multiple small units, yet they are part of a much large migratory process. Overall, diaspora consists of large-scale migration into inhabited communities where immigrants maintain persistent connections and aspects of their identity related to their natal homelands (Clark 2001; Clark et al. 2013; Lyons 2003). Key traits of this type of migration include, relatively large population displacement, long distance movement, maintenance of migrant interaction, zones of heterogeneity, and transformation of local population trajectories (Mills 2011).

Demographic studies indicate that over a 500-year time span (AD 500–1000) populations in the Southwest had steadily increasing birth rates with some fluctuation until around AD 1300 when they began to decline (Hill et al. 2004; Kohler and Reese 2014). Environmental changes and fluctuations pushed previously dispersed populations into aggregated communities situated in confined core areas with fertile alluvium for agriculture (Alder 1996; Lipe 1999; Wilshusen and Ortman 1999). San Juan River Animas (Pueblo I) sites are located south of the modern town of Durango, Colorado, and some suggest several different groups resettled in the area based on distinctions in architecture, mortuary practices, and biodistance analyses (Potter et al. 2010; Potter and Perry 2011). Occupation lasted until A.D. 800 when climate fluctuations again forced

people out of the area (Charles et al. 2006; Gooding 1980; Lipe 1999; Potter 2010). Some of these people potentially migrated west into the Dolores McElmo and Northern San Juan (Middle) sub-regions where substantial village aggregation was occurring.

Villages did not form in the Southern San Juan sub-region, which encompasses Chaco Canyon, until after AD 875 (Wilshusen and Van Dyke 2006). Migration is an essential part of understanding the establishment, organization, and abandonment of great house settlements in Chaco Canyon, which served as a stratified economic and political center until its abandonment by AD 1150 (Clark and Reed 2011; Judge and Cordell 2006; Lekson 2006). After AD 1050, Chaco Canyon communities became more linked to settlements to the north along the San Juan River. Material evidence points to migration out of Chaco Canyon north into the Middle San Juan during the late 1000's and early 1100's (Clark and Reed 2011).

As birth rates plateaued in the region around AD 1000 in the region, people began to exploit smaller territories, or internal frontiers, more intensively as a viable strategy for population continuity (Kohler and Reese 2014). In the Southwest, internal frontiers were often located between densely occupied villages and serve as contact points for trade and travel as transitional brokerage zones where they mediate interactions between otherwise disconnected communities (Peeples and Haas 2013). These settlements to the north of Chaco may have originated as Chacoan "internal frontiers", with populations shifting and re-aggregating to the north. From the late thirteenth through the mid-fifteenth century, large-scale population displacements, including diasporas from the Northern San Juan (including Mesa Verde) and the Northeastern Arizona (Kayenta) sub-regions, ushered in changes in how people interacted and organized themselves across the region (Ahlstrom et al. 1995; Clark 2001: Hill et al. 2004; Lekson et al. 2002; Lyons 2003; Woodson 1999). Substantial archaeological work addresses

whether people immigrated from Mesa Verde to the northern Rio Grande sub-region (Cameron 1995; Kohler and Varien 2012; Ortman 2012) and from Northeastern Arizona to south to the Arizona Mountains and settlements in the San Pedro River Valley (Haury 1958; Lindsay 1987; Lyons 2003; Stone 2003). It is inferred that people migrated from Mesa Verde to the Rio Grande based on demographic, linguistic, and biodistance evidence (Ortman 2012). Material elements and indicators from the Northern San Juan (Middle) are not identified in the northern Rio Grande, which has led some to argue that local demographic increase was due to internal growth within the region rather than migration (Boyer et al. 2010; Lakatos 2007).

Movement of non-local people from the Northeastern Arizona (middle) sub-region into the Arizona Mountain and the Mogollon Rim altered previous migration patterns as people organized themselves into larger settlements (Reid et al. 1996). Extensive material and architectural evidence at large Mogollon Pueblo sites located in the Arizona Mountains, such as Point of Pines Pueblo, led archaeologists to infer that immigrant enclaves from the Kayenta sub-region co-resided with locals by AD 1265 (Haury 1958; Lindsay 1987). As some places in the northern and southern Little Colorado drainage system became depopulated and others grew, there was a widespread shift in community organization and regional settlement patterns among the Rio Puerco of the West, Zuni River, El Morro Valley, and Eastern Little Colorado (Cibola) (Peeples 2011; Schachner et al. 2011). The southern Cibola sub-regions were inferred to be the destination for many migrating people from outside of the region, which would include the Eastern Little Colorado sub-region in this study, whereas the north-eastern populations remained more localized (Peeples 2011).

Figure 3 illustrates migration scenarios inferred from processes of migration into internal frontiers, and diaspora among the sub-regions of the northern and central Southwest.

Aggregation and migration into internal frontiers are expected to be evident among sub-regions as natal (origin) and population sub-sets with close affiliation and higher and lower than expected observed variance, respectively. Additionally, I test expectations of diaspora south from the San Juan and Northeastern Arizona sub-regions. If diasporic migration occurred as proposed, then we should expect to observe close biological affiliation between origin and destination communities due to migrant co-residence with locals and higher than expected variation due to increased gene flow. Alternatively, if higher than average gene flow occurred between these groups because of their close geographic proximity, then we should expect to observe close biological affiliation across their associated skeletal samples following the isolation by distance.

Coalescence and Reorganization

Population upheaval and resettlement requires people to form new relationships and reorganize themselves. Coalescence is a term applied to this process that refers to community reorganization and the formation of diverse aggregated groups. When paralleling environmental change and degradation, coalescence is identified as contributing to demographic decline (Hill et al. 2004). A demographic study of Oaxaca Valley population history spanning 3,500 years illustrates how demographic transition processes have biological and political causal factors. Biological factors operate over space and time and involve entire populations that vary by adaptive range or niche space, and they are at times closely coupled with political-economic cycles (Kowalewski 2003). Migration is a catalyst for coalescent communities to form, as it generates economic pressure and social disruption often at a large scale (Hill et al. 2004). In this way, social reorganization found in coalescent communities brings diverse people in contact where they have increase opportunities to co-reside and reproduce, which affects the biological structure of the community overtime.

Migration during the Late Period (AD 1400–1700) is characterized by depopulation in some areas, aggregation in others, and the nucleation or coalescence of diverse people, which altogether constituted regional reorganization (Peeples 2011; Spielmann 1998). Consequentially, birth rates began to decline rapidly in the region beginning in 1300. Kohler and Reese (2014) find considerable oscillations and variability in the juvenility index (across sub-regions through 2,500 years beginning in 1000 BC) in the Southwest. Juvenility index is calculated as the number of individuals between 5–19 years of age divided by all individuals 5 years or more in age, which is found to be a simple paleodemographic indicator strongly correlated with crude birth rate or natality. Sub-regions included within the Late Period of this study can be divided into those ethnographically and archaeologically categorized as Western (Zuni River, Northeastern Arizona, and Middle Little Colorado) and Eastern Puebloan (Rio Grande, Lower Puerco, Pecos, Galisteo Basin, Central New Mexico) (Bernardini and Fowles 2011; Duff 2002; Eggan 1950). Arizona Mountains, Lower Salt, Lower Gila, and Tonto Basin sub-regions are located to the south and were only occupied until the first half of the fifteenth century. Bernardini (2011) argues that ethnographers have overstated Western (Hopi, Zuni, Acoma, Laguna) and Eastern (Tewa, Tiwa, Towa, Keres) differences in social organization, and that, more parallels exist in kin-based structures, dual organization, and ritual sodalities.

In the Tonto Basin, an influx of settlers from surrounding sub-regions led to a shift from dispersed settlements to more aggregated settlements in thirteenth century. Clark (2001) finds evidence that Tonto Basin roomblocks were built by immigrants from northern sub-regions including Northeastern Arizona, and that migrants and local people co-resided. Ancestral Hopi villages (AD 1260–1400) located the Middle Little Colorado were comprised of people primarily from the Hopi Mesas (Barker 2017; Lyons 2001, 2003). Some migrants from Homol’ovi likely

rejoined communities on Antelope Mesa, such as Awat'ovi and Kawàyka'a, in Northeastern Arizona that were growing during this time (Adams 2001).

The Lower Salt and Lower Gila River drainages of southern Arizona held Hohokam settlements characterized by irrigation canals, monumental architecture (ball courts, platform mounds) and substantial long term sedentism. Population decline followed coalescence that began in the late thirteenth century, and over the course of one hundred and fifty years eventually led to small remnant groups that could not maintain their vitality in southern Arizona which was depopulated by AD 1450 (Hill et al. 2004). These small remnant groups left the area or shifted to a less archaeologically visual lifestyle. Reasons for abandonment of the sub-region range from conflict and disease to environmental degradation (Abbott 2003; Doyel 1981, 1991; Gregory 1991). Emigration may have contributed to the population decline, particularly if migrants were reproductive-aged adults (McClelland 2015), or if changes in the ratio of births to deaths contributed over the long term to declining population size (Van Gerven and Sheridan 1994).

During the subsequent Protohistoric period (AD 1450–1540), migrations were likely directed north to ancestral Hopi and Zuni settlements in Northeastern Arizona and along the Zuni River (Duff 2002; Peeples 2014). Hopi villages likely included migrants from the Kayenta cultural region to the north who moved south during the later thirteenth century. In the later fourteenth century, immigrants moved back north to the Hopi Mesas from areas within the Middle Little Colorado (Adams and Duff 2004; Bernardini 2005; Lyons 2003). Zuni River settlements show strong archaeological evidence of sociocultural change from the 1300s to the 1400s, particularly in settlement patterns, architecture, ceramic technology, and burial practices (Kintigh 2000). Large villages in the Zuni area experienced an increase in the number of cremation burials, which account for 30% of the mortuary features at Hawikku and Kechiba: wa

(Kintigh 2000). Before the Protohistoric period, cremations were not found in this sub-region, and here they were discovered clustered in discrete cemetery groups. Protohistoric villages within the Zuni River (Late) sub-region represent groups with diverse origins, or uneven migration of new arrivals (Howell and Kintigh 1996; Peeples 2014). Some suggest that Lower Salt populations may have been direct ancestors to the Protohistoric Zuni people due to their commonalities in cremation burial practice (Brunson 1989; Cushing 1890), and others have linked sites in the Point of Pines area, south of the Mogollon Rim, to Protohistoric Zuni sites based on similar treatment of cremation vessels (Robinson and Sprague 1965). Thus, the influx of people into Zuni River settlements practicing cremation may be reflective of migration from people originating in the Lower Salt, Lower Gila River valleys, and Arizona Mountains sub-regions of southern Arizona.

The introduction of glaze ware pottery in Rio Grande communities has been partially attributed to migration from the west, with production beginning approximately AD 1275 as it has also been identified in the Arizona Mountains and Zuni River sub-regions (Habicht-Mauche 2006). People originating in the Western Pueblos (Hopi and Zuni) likely introduced glaze technology into the Rio Grande draining from the Rio Puerco of the East (Lower Puerco) (Eckert 2008). The local population at Pottery Mound had a long history of residence before immigrants entered the area in the late 1200s and early 1300s. Stronger evidence for immigrants from the Zuni River (late) sub-region is present at Hummingbird Pueblo compared with Pottery Mound. Other evidence suggests that there was migration to Pottery Mound from the Hopi mesas (Northeastern Arizona (late)), including nonlocal pottery traced directly to the Hopi Mesas, similarity of Hopi designs and mural designs at Pottery Mound, and some untempered glaze-painted pottery with Hopi designs Pottery Mound (Eckert 2008; Hibben 1975). Sikyatki style

was abundant at Pottery Mound as shown in multiple kiva murals at the site. Awat'ovi and Kawàyka'a, located on Antelope Mesa, also have Sikyatki style kiva murals dating to the late 1400s to early 1500s. These were diverse communities where connections through migration was clearly possible with Rio Grande communities (Hargrave 1935, 1937; Hays-Gilpin 2013; Hays-Gilpin and LeBlanc 2007).

In 1540, Francisco Vasquez de Coronado traveled into what is now New Mexico, and encountered the Zuni village of Hawikku. The eastern Southwest sub-regions of Galisteo Basin, Central New Mexico, Northern and Middle Rio Grande experienced the first Spanish contact in the Southwest along with the colonization of the Pueblos in New Mexico in the early 1600's (Hammond and Rey 1953). During this time, men were commonly exploited for labor and forced to transport items such as pinon nuts, corn, salt, along with hides over long distances which changed local population structure and organization (Spielmann 2006). Larger border pueblos, including Pecos and Gran Quivira, began intensifying relationships with the Plains (Leonard 2006). The Salinas Pueblo province in the Central New Mexico sub-region is located approximately sixty miles southeast of Albuquerque was formed by northern (Manzanos) and southern (Jumanos) settlement clusters. Friars established large mission churches at the villages of Abo and Quarai in the north which were active until AD 1670. To the south, Gran Quivira was more remotely located, and a third friar stayed for one year before returning to Zuni. Gran Quivira did not have a mission re-established until the 1660, when it became a vista of Abo pueblo (Spielmann 2006). Burial practices at Gran Quivira exhibited similar cremation ratios as were observed in Zuni River (late) Protohistoric villages but did not occur until much later, at AD 1550 (Hayes, Young, and Warren 1981). Communities along the Rio Grande that specialized in glaze ware manufacture retained local autonomy through their choices related to resource

procurement, technology, and design (Huntley et al. 2007). Large scale disruption of Puebloan life on the Rio Grande during the 1600s, including disease epidemics and the Pueblo Revolt of 1680 led to a post revolt period (AD 1683–1694) when women used ceramics to promote revitalization. Eckert (2006) states that post-Revolt societal reconstructions, land grants, and other settlement characteristics led to the end of glaze pottery production. Glaze ware bowls and jars were manufactured south of Sante Fe until AD 1680 (Spielmann 1998).

Figure 4 illustrates vertical and transverse migrations associated with population coalescence and reorganization. During the Late Period (AD 1400−1700) people are inferred to have moved vertically within their associated Western and Eastern areas, yet also across the region and into coalesced settlements comprised of diverse people from multiple origins, such as from the Lower Salt to the Zuni River (Late) sub-regions, and Rio Puerco of the East (Lower Puerco), Zuni River (Late), and Northeastern Arizona (Late) sub-regions based on archaeological evidence. Although it is possible that biological connections between the eastern and western sub-regions may be identified, it is also likely that Eastern sub-regions may exhibit distinct variation and affiliation patterns due to differential impacts of European contact on the population structure of sub-regions included in the Late period.

MATERIALS AND METHODS

Eight craniofacial measurements were collected and compiled from 1,299 crania representing 28 sub-regions across the North American Southwest. Data were collected and compiled in two ways, 1) direct manual collection of cranial measurements with spreading and sliding calipers by the author, and 2) compilation of cranial measurements through personal communication with other analysts and from publications. Cranial measurements were organized in a database along with associated burial identification, site, site location, and sex. Individual

cases were grouped into one of 28 sub-regions based on archaeological site location and temporal period (Table 1; also see supplementary materials for analysts and sites included within each sub-region).

Analyzing craniofacial morphology within a population history framework allows for robust interpretations of migration and gene flow in the past. Cranial morphology is widely recognized as moderately heritable (Carson 2006; Martinez-Abadiás 2011; Reyes-Centeno et al. 2017), and functions as a proxy for allele frequencies under an additive effects model of quantitative genetic inheritance (Cheverud 1988; Konigsberg 2000). Under this additive model, phenotypic similarities are the sum of weighted genetic and environmental influences. The additive component of variance contributes to the phenotypic resemblance between related individuals (Cheverud 1988). Human cranial morphology exhibits some functional and developmental plasticity, yet it is not considered to be enough to erase signatures of biological relatedness (Relethford 2004; Von Cramon-Taubadel 2009).

Relethford and Blangero (1990) state that when populations exchange mates, within-group variation and genetic distance deviations indicate differences in average gene flow. Populations with higher variation than expected are inferred received greater gene flow, whereas those with less variance than expected received less gene flow (Relethford and Harpending 1994; Relethford 1996). Gene flow eventually acts to biologically homogenize migrant and local groups, resulting in closer genetic, and therefore phenotypic, relationships and affinity. However, groups that do not exchange mates become more dissimilar at a rate determined by population size (Stojanowski and Schillaci 2006). Phenotypic variation and the calculation of biological distances (measures of potential relatedness) provide a framework for inferring population structure and history to provide insight into how gene flow affects small populations (Knudson

and Stojanowski 2008; Relethford 1996; Stojanowski and Buikstra 2004). Therefore, by analyzing both variance and affinity, inferences regarding process such as migration have implications for testing archaeological inferences based on material evidence alone. I argue that one of the best ways to incorporate the biological expectations for archaeological migration scenarios to understand past human group dynamics is through a population-history approach, which incorporates the cumulative effects of biological interactions over time.

Alternately, the isolation-by-distance model hypothesizes that random mating is limited and constrained by distance, so that individuals encountering others in relatively close physical distance are more likely to mate than those farther away, leading to genetic similarity as a function of geographic distance (Wright 1943). Neutral variation found in cranial morphology corresponds with patterns of isolation by geographic distance (Harvati and Weaver 2006; Konigsberg 1990). Indicators of isolation-by-distance are expected if people were experiencing limited long-distance migration (or were relatively non-mobile) and inter-population gene flow was restricted to adjacent sub-regions.

Data collection and preparation

Data tested here include eight standard linear facial measurements including upper facial height, nasal height and breadth, orbital height and breadth, 133axilla-alveolar breadth and length, and bizygomatic diameter (Buikstra and Ubelaker 1994). These measurements were chosen because they were most frequently represented, providing the largest sub-region sample sizes. Furthermore, multiple studies have demonstrated a significant correlation between facial morphology (particularly the upper face) and neutral genetic variation (Roseman 2004; Smith 2009; Von Cramon-Taubadel 2009). They also allow for the inclusion of culturally modified

crania, largely avoiding the effects of cranial modification due to cradleboarding (Kohn et al. 1995). Crania with at least 50% of the measurements preserved were included in the analysis. All other data included in this study were compiled from various published sources and through personal communication (see sources listed in Table 2, and supplementary materials Table 1). Hrdlička (1931) published a seminal data set of Southwest linear craniometric measurements drawn upon by numerous biodistance analysts, and many groups he measured were included in this study.

Preservation issues make missing data estimation a standard data preparation step with bioarchaeological samples (D'Amore et al. 2010; Von Cramon-Taubadel and Pinhasi 2011). Multiple imputation is used with an algorithm based on the Markov Chain Monte Carlo (MCMC) to obtain missing values sampled from a normal distribution. Male and female data are standardized by unbiased standard deviation (z-scores) to eliminate the effects of size due to sexual dimorphism. In addition, this allows for pooling sets of male and female data which maximizes the small sample sizes (Carson 2006).

Relative population size and narrow-sense heritability (h^2) are two parameters estimated for statistical analyses using RMET 5.0 software. Population size estimates were taken from previous biological distance studies conducted in the region (Ortman 2012; Peeples 2014) based on regional archaeological population size estimations (Adams and Duff 2006; Alder 1996) to account for differential effects of genetic drift on phenotypic variance of small populations. Parameters for Early Agricultural, Eastern and Western Basketmaker II, and many of those groups dating pre-AD 1000 were estimated based on time-depth and in proportion to other sub-regions included in both Model 1 and Model 2 that include these earlier sub-regions. Narrow-

sense heritability (h^2) was set to 0.55, following recent craniometric biodistance studies conducted in the region (Schillaci 2003; Schillaci and Stojanowski 2003; 2005).

One assumption this study makes is that archaeologically defined sub-regions can be used to model phenotypic variation as a panmictic (randomly mating) biological population. Following Ortman (2012), human skeletal remains recovered from archaeological sites are considered samples of lineages rather than population samples because not all people included in the sample were alive at the same time and mating probabilities were not equally distributed within in sub-region. Given these caveats, if unequal effects of drift are controlled for, cranial morphology has shown to be moderately heritable. Ortman (2012) argues that patterns of variation are reasonable as a random sample of individuals from several generations and do not pose a significant problem.

ANALYSIS

Phenotypic variances and biological distances among 28 sub-region groups are calculated following the Relethford-Blangero analytic framework (1990) using a relationship matrix, or R-matrix. An R-matrix (r_{ij}) is a standardized variance-covariance matrix of allele frequencies within a tested population sample. This framework follows the premise that when populations exchange mates at an equal frequency, within-group variation and genetic distance to the centroid should be linear and any significant deviations indicate differences in average gene flow. Therefore, groups with higher variation than expected are inferred to have received greater than average gene flow, whereas groups with less variation than expected received less than average gene flow (Relethford 1996; Relethford and Harpending 1994). This analysis is conducted three times to test the proposed migration processes within three temporal periods.

The R-matrix is converted into an unbiased R-matrix to account for small and widely divergent sample sizes and sampling error (Relethford et al. 1997; Steadman 2001). Weighted diagonals of the R-matrix are used to produce measures of Wright's F_{ST}, or population differentiation around the centroid (Relethford and Harpending 1994). This is useful for comparing regional total population differentiation and variation with other samples derived from cranial metric traits. Significance of residual variance and F_{ST} is conducted by jackknifing across all variables and conducting a two-tailed Student's t-test with the calculated standard error.

Referred to as the D-matrix or biological distance matrix (Relethford and Blangero 1990), these distances are converted from the unbiased R-matrix values as D-matrix distances (d_{ij}^2) are relative to 0 or 1, with groups less similar being further from 0 and groups more similar being closer to 0. Large genetic distances among one or many groups may indicate influences due to population size or relatively greater admixture with groups outside the immediate group (Relethford 1996). Principal Coordinates Analysis (PCA) is conducted from the scaled R-matrix, which was scaled by the square root of estimated proportional population weights. The first two eigenvectors scaled by the square root of their eigenvalues are plotted to visualize phenotypic similarity and affinity among site groups tested. Proximity observed between sub-regions displayed on PCA plots are interpreted as reflecting biological relatedness or affinity.

Matrix correlation and Mantel tests

The final step is to test if biological distances are influenced by geographic distance. Distances (km/mi) were estimated between each of the sub-regions most estimated distant points to account for the longest possible distance traveled and constructed into a matrix for each

model. Mantel tests are designed to test significant correlations between matrices and were conducted with each model to test correlation significance between biological distances (D-matrix distances) and geographic distances between sub-regions. PASSaGE 2 was used to test these matrix correlations (Rosenberg and Anderson 2011). Outcomes of these analyses demonstrate if variation was patterned by geographic distance following the isolation by distance model.

RESULTS

Early Period Results

The Relethford-Blangero analysis of Early period sub-regions (Table 3) finds significantly more than expected within-group phenotypic variance in the Sonoran Desert and Northern San Juan (Early) sub-region samples. Significantly less than expected variance is present in the Northeastern Arizona (Early) sub-region. Unbiased F_{ST} (genetic differentiation) for the combined site groups did show significant variance from 0 (F_{ST}= 0.2644; p = <.0001). This indicates that the Sonoran Desert and Northern San Juan (Early) sub-regions experienced higher than average gene flow likely due to having high rates of in-migration, or from the founding groups having diverse origins. PCA results (Figure 4) includes the x-axis representing Eigenvector 1 accounting for 84.5% percent and the y-axis representing Eigenvector 2 accounting for 10% of the total variance present among the four sub-regions included in the Early period (94.5% total). Close phenotypic affinity is exhibited between the Northeastern Arizona (Early) and Sonoran Desert sub-region samples with little variation on the x or y-axes. The Northern San Juan (Early) sub-region sample, in addition to significantly high phenotypic variance, is phenotypically distinct from the other sub-regions tested. Mantel test results indicate

that there is not a significant relationship ($p = 0.704$) between geographic and biological distance among Early period groups.

These results support the inference that migration occurred from the Sonoran Desert northward to the Northeastern Arizona (Early) sub-region. Since the Northeastern Arizona (Early) sub-region sample demonstrates significantly low variance, it is likely that this was a destination for migration from the Sonoran Desert before AD 500, with the migrating population exhibiting the effects of genetic drift. The Western San Juan sub-region does not show close biological affiliation with other sub-regions but is more closely related to the Northeastern Arizona (Early) and Sonoran Desert sub-regions compared with the Northern San Juan (Early) sub-region. Geographic distance is not significantly correlated with the biological distances of sub-regions included in the Early period, indicating the isolation by distance did not substantially influence variation.

Middle Period Results

For the Middle period, Unbiased F_{ST} ($F_{ST} = 0.0649$; $p = <.0001$) indicates variance significantly different than 0 among twelve groups tested, although this is much less than what is calculated for the Early period. Relethford-Blangero analysis indicates that variance of the San Juan Animas, San Juan Piedra, and Dolores McElmo are not significantly high or low copared to average expected variance (Table 3). The Dolores McElmo sub-region appears to be relatively distinct with the closest affinity being with the San Juan Piedra and the Northeastern Arizona (Middle) sub-regions. The San Juan Animas and the San Juan Piedra sub-regions show relatively close biological affinity to one another, as well as with the Northern San Juan (Middle) sub-regions when compared with other sub-regions included in the Middle period. Variance of the

Northern San Juan (Middle) sub-region that includes Mesa Verde is not significant and shows close biological affinity with the San Juan Animas sub-region (Fig. 4).

These results suggest that migration was likely more localized along the San Juan River drainage, although the Dolores McElmo sub-region shows some affinity with those living in Northeastern Arizona (Middle). This is possibly due to aspects of shared population history such as shared ancestral lineage or migration from the Dolores/McElmo to the Northeastern Arizona (Middle) sub-region due to significantly high variance observed that is indicative of higher than average migration and gene flow (Table 3).

Significantly low within-group variance was identified among the Southern San Juan (which includes Chaco Canyon), Middle San Juan, and Rio Puerco of the West sub-regions. The Southern San Juan and the Rio Puerco of the West show centralized biological affinity, and group very closely with the Zuni River (Middle) sub-region (Fig. 4). The Middle San Juan sub-region has significantly low variance and is exceptionally biologically distinct on the x-axis which accounts for 59% of the total variance graphically represented. Expectations are only partially met with Model 2, as support is not provided for close biological affiliation between those occupying the Middle San Juan indicating that it is unlikely substantial gene flow occurred into this sub-region from the others included in the Middle period. However, the Southern San Juan sub-region sample shows relatively close affiliation with Northern San Juan (Middle) sub-region indicating possible gene flow in support of migration between Mesa Verde and Chaco Canyon settlements.

Significantly more than expected within-group phenotypic variance is evident in the Arizona Mountains and Northeastern Arizona (Middle) sub-regions (Table 3). Both sub-regions show distinct biological affinity compared to the other sub-regions (Figure 4). The main source

of variance between these two sub-regions is on the x-axis which only accounts for 20.8% of the total variance present, as the sub-regions do appear to show close affinity on the y-axis. The high variance in both sub-regions and the relatively close, yet distinct, biological affinity provide some support for the expectation that these two sub-regions would show close biological affinity due to Kayenta migrant co-residence with Mogollon Rim Pueblo locals. It is very likely that both sub-regions experienced outside migration, possibly from the Dolores McElmo in the Northeastern Arizona (Middle) sub-region and from outside sub-regions not included in this period. Following expectations, close biological affinity is observed between the Little Colorado River draining sub-regions, including the Rio Puerco of the West, Zuni River (middle), El Morro Valley, and Eastern Little Colorado likely due in part to geographic proximity (isolation by distance) although this could not be verified with Mantel test results as they did not indicate a significant correlation between the biological and geographic distances.

Late Period Results

The Relethford-Blangero analysis testing the Late period (Table 3) includes thirteen sub-regions to examine the interconnected migration patterns into the AD 1500s. The results presented below indicate differing levels of migration and gene flow occurring across the North American Southwest at this time (AD 1150–1680). The sub-regions exhibiting significantly lower within-group variance all date to the latter half of this time range, immediately before or during the historic period. Significantly higher than expected within-group variance indicates a likely migration locale primarily occupied during the earlier part of this time range. Significantly high variance is observed in the Tonto Basin sub-region, however neither significantly high or low variance is observed in the Lower Salt, Lower Gila, and Middle Little Colorado sub-regions.

The Lower Salt and Lower Gila show very close biological affiliation (Figure 5) following expectations, they also show close affiliation with Middle Little Colorado, Northeastern Arizona (Late), and Middle Rio Grande sub-regions.

Results indicate that Central New Mexico, Zuni River (Late), Pecos River, and Northern Rio Grande have significantly lower within-group variance than expected. However, the Arizona Mountains, Rio Puerco East, and Galisteo Basin sub-regions exhibit significantly higher within-group variance than expected. Of these sub-regions, three stand out as more distinct than the rest, including the Arizona Mountains (similar to Middle period results), Pecos River, and Rio Puerco of the East. Support is not provided for the expected biological relationships connecting the Rio Puerco and Northeastern Arizona (Late) sub-regions. However, substantial support is provided for the Rio Puerco (comprised of individuals buried at Pottery Mound) as a locale that attracted migration due to the significantly high variation. Migrants possibly came from sub-regions or sites outside of those that were included in the Middle period. The Zuni River (Late) sub-region shows very close biological affinity with the Galisteo Basin sub-region, as well as the Northern Rio Grande. This supports the idea that migration cross-cut the region and bridged Western and Eastern Pueblos, and that eastward migration may have accompanied the movement of glaze ware pottery during this time. Overall, the results follow expectations that migration and gene flow cross-cut the geographically distinct (east-west) portions of the North American Southwest after AD 1450. Unbiased F_{ST} (F_{ST} = 0.0601, p =0.0001) shows relatively similar diversity encompassed in Late period compared with results testing the Middle period. Mantel tests results indicate near significant correlation between biological distances and geographic distances (p = 0.080) suggesting that geographic distance played a more important role in admixture among groups.

DISCUSSION

It is important to recognize that multiple interconnected migration scenarios impact population histories in a combination of ways. The results of the analyses presented provide strong support for archaeological inferences that migration closely follows patterns in material culture in many cases. Biodistance evidence supports expectations following colonization of open landscapes, internal frontiers, diaspora, and reorganization by applying the expectations of these models to the population histories of the Southwest inferred from archaeological evidence. There are robust biological signatures to indicate migration from the Sonoran Desert to Northeastern Arizona (Early) sub-region shown in the Early period and the Zuni River (Late) with the Galisteo Basin and Northern Rio Grande in the Late period. A major element of the transformative process of migration is altering how people organize themselves socially, which also has long-term oftentimes inadvertent biological consequences. The colonization of open vacant land, migration into internal frontiers, and long-distance diaspora, and subsequent reorganization are scenarios characteristic of the prehistoric Southwest that shaped both the cultural and biological composition of contemporary Native peoples of the region. By examining variance alongside biodistance results, this research sought to refine inferences regarding microevolutionary processes in the region over time which reflect population-histories associated with groups as a given point in time and space. For example, variance levels of the closely related Northeastern Arizona (Early) and Sonoran Desert differ significantly indicating that processes of genetic drift and gene flow were functioning together in this migration scenario, with the possibility that a sub-set of the population migrated from the Sonoran Desert to Northeastern Arizona (Early) representing a sub-set of the variation present in the Sonoran Desert that migrated and resettled in Northeastern Arizona. Distinctions between variance and

biological distances help identify which sub-regions received relatively more people moving in, and how they were related.

The results presented in this study do not support the idea that generalized continuity influenced widespread biological relatedness across the Southwest because sub-regions exhibit drastic differences in biological affinity and variance levels. The results instead support the hypothesis that ancestral Southwest populations originated from multiple distinct founding lineages which is also supported by multiple other biodistance studies in the region (Corruncini 1972; LeBlanc et al. 2008; LeBlanc et al. 2007; Ortman 2012; Turner 1993). However, on the sub-region level evidence presented here does not directly align with that reported by Akins (1986) and Schillaci (2003), who found a highly variable population buried at Chaco Canyon. Schillaci and others (2001) found that two groups inhabited Pueblo Bonito, with separate affinities to groups outside of Chaco Canyon. Durand and others (2010) find close similarity between Chaco Canyon and the Salmon Ruin Totah enclave and argue for the presence of both local and immigrant groups at the Salmon great house in the Middle San Juan sub-region. The results presented here suggest that those from the Southern San Juan sub-region are more closely related to people buried at the Northern San Juan (Middle) sub-region compared to those in the Middle San Juan sub-region. People representing lineages buried in the Middle San Juan sub-region possibly originated from a Southwest sub-regions not included in Model 2, or from outside of the region.

This study also provides evidence indicating Western Basketmaker II people living in Northeastern Arizona and Early Agricultural people from the Sonoran Desert were related, likely due to a northward migration. Eastern Basketmaker II groups from the Northern San Juan (Early) show high variance and divergent morphology compared with both Western Basketmaker II and

Early Agricultural groups providing support for the existence of multiple lineages. Mortuary practices, including burying individuals alone, or with others, head orientation, and burial artifact association all occurred at different frequencies between Eastern and Western groups living in the Northern San Juan (early) and Northeastern Arizona (early) and Western San Juan sub-regions (Mowrer 2006). These results provide potential support for the inference that Eastern Basketmaker II people descended from indigenous groups that were adapted to high-elevation living (Charles 2000; Matson 1991).

At the other end of the temporal spectrum, the results of this study did not to support an Eastern and Western Pueblo dichotomy structuring the local reorganization process during the Late period. Ethnographically, Western Pueblo groups (Hopi, Zuni, Acoma, Laguna) in anthropological classifications are defined as exhibiting exogamous matrilineal clan social organization with matrilocal post-marital residence patterns (Eggan 1950). Eastern Pueblo groups along the Rio Grande and in other sub-regions of northern and central New Mexico were based primarily on systems of dual organization with ritual sodalities, including kiva-moiety organization that provided groups with a place in the ceremonial life of the pueblo (Bernardini and Fowles 2011). So although social organization differed in ways between the eastern and western portions of the Southwest, admixture continued to occur across the region during this time.

Archaeological evidence suggests the Western Pueblo complex was abandoned in the late AD 1300s (Duff 2000). The establishment of Zuni towns as, reported through traditional knowledge, includes descriptions of diverse migrations where people interacted along the Zuni River (Ferguson 2007). Migrants most likely arrived in groups comprising multiple households of people related through lineages. Peeples (2014) argues that the levels of variance observed

among the Zuni indicates that even if outside gene flow did account for a portion of the genetic diversity at, for example, Hawikku, there was also a robust biological relationship among earlier populations in the Zuni sub-region. The results presented here demonstrate higher than expected variance, and close affinity between Zuni and groups from the Galisteo Basin. In contrast, the Eastern pueblos (located along the Rio Grande River) generally exhibit large moiety kivas, and Tewa-speaking people's kinship patterns are based on endogamous organization centered on dual winter and summer sodalities (Ware and Blinman 1998). However, Western and Eastern Pueblos appear more integrated biologically than distinct. The Zuni River Zuni, Rio Puerco East, and Galisteo Basin likely served as migration and integration hubs among the Western and Eastern Pueblos. For example, in the AD 1550s people at Gran Quivira began practicing cremation. This has been attributed to a possible influx of population from the west (Zuni area) (Cordell 1995). Population growth in the late Salinas pueblos is likely due to a combination of increased fertility and aggregation into fewer nucleated sites (Rautman 2014). Furthermore, Mantel tests reveal closer geographic distance correlation with affinity patterns during the Late period, indicating that previous migration and ancestral lineages (population-history), more complex social organization based on nearest-neighbor post-marital residence, and eventually European contact together shaped population structure after AD 1550.

Tracing migration through physical characteristics (including skeletal and dental morphology, isotope, or aDNA) is challenged as assuming intergenerational stability in socially defined migrant groups. However, the biological implications for reconstructing migration process through vertical descent and horizontal interaction is situated on the population level, rather than in the identification of separate migration situations (Bellwood 2013). Von Cramon-Taubadel and Pinhasi (2011) found a complex mosaic process of dispersal and changes in

admixture over time characterized the spread of agricultural subsistence practices into Europe from Southwest Asia, rather than local development of agricultural subsistence practices by hunter-gatherer groups. There was relatively less gene flow between farming and hunter-gatherer lineages, indicating that migration patterns in more remote regions of Europe involved a complex pattern of diffusion referred to as demic diffusion. Demic diffusion occurs with intermarriage between adjacent settlements and genetics spread by local processes that do not necessarily involve long-distance migration but is characterized more by spouse movement locally within the settled landscape.

In a study of admixture as a microevolutionary agent, Martinez-Abadias et al. (2006) find that cranial morphology of admixed (early and late) populations from Amerindian and Spanish contact groups in Mexico's Central Valley do not show an exactly intermediate position, but are positioned between both ancestral populations, with the earlier admixed group showing closer affinity to the Amerindian centroid and the later showing closer affinity to the Spanish centroid. These patterns are also reflected in this study, but on a smaller scale prior to AD 1540. Frankenberg and Konigsberg (2011) used simulated data from six quantitative traits from two demes (closely biologically related groups) to model two extremes of complete continuity (no migration) and complete replacement (all 100 individuals). They specifically examine how big a migration event needs to be to be biologically detectable, and how long after the migration event will it be detectable with a small population size and drift by testing different scales of migration (0 – 100 individuals) and length of post-migration drift (number of generations 1– 50; 25– 1,250 years). Their results suggest that migrants will be difficult to identify biologically unless the proportion of the migrations to local population is very high and if trying to detect migration. All in all, their study highlights that migration will have small or undetectable biological effects

when measured in terms of quantitative traits if population sizes and migrant totals are small, if migration is a single event, and if genetic drift has a long time to operate.

CONCLUSIONS

This study demonstrates that intra-regional migration and differential gene flow impacted population structure and history after the formation of agricultural communities in the North American Southwest. Differential migration and gene flow processes occurred across 3,800 years of occupation and on multiple scales (site, sub-region/district, and regional level). Eight of the 28 archaeologically-defined sub-regions are distinguished by significantly higher than expected variance, indicating these locations served as centralized hubs for migrants. Several sub-regions including the Northern San Juan (Early), Arizona Mountains, and Rio Puerco of the East (Lower Puerco) exhibit significantly high variance and distinctive biological affinity indicating the potential of in-migration from outside areas not included in this study.

This study highlights the importance of a population-history approach, examining within-group variance, biological distances, and affinity in a diachronic approach in order to emphasize the biological impact different migration processes had on past populations. Migration was a crucial component influencing technological and social organization before, during, and after European contact. Colonizing unoccupied locales, movement into and settlement of internal frontiers, and diaspora are all recognized types of migration characteristic of the region. The data reported here indicate that after AD 1400, post-marital residence patterns and geographic proximity played a greater role in how and where people migrated. Applying biological distance analyses to craniofacial morphology is a nondestructive approach that adds depth to our understanding of how migration affected human organization in past populations.

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FIGURE 1: Map of 28 sub-regions included in this study

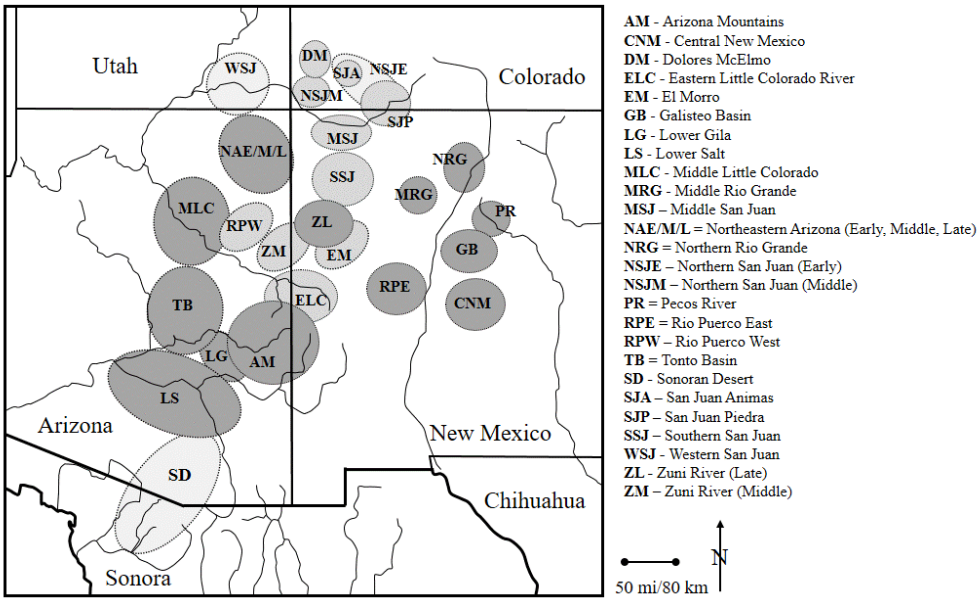

FIGURE 2: Early period (2100 BC–AD 500) colonization of open landscapes

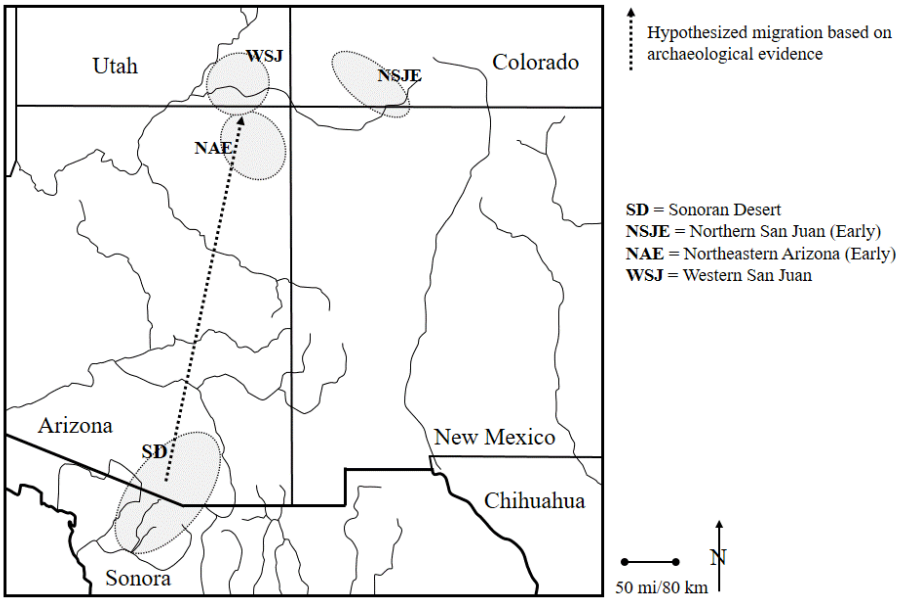

FIGURE 3: Middle period (AD 700–1400) migration into internal frontiers and diaspora

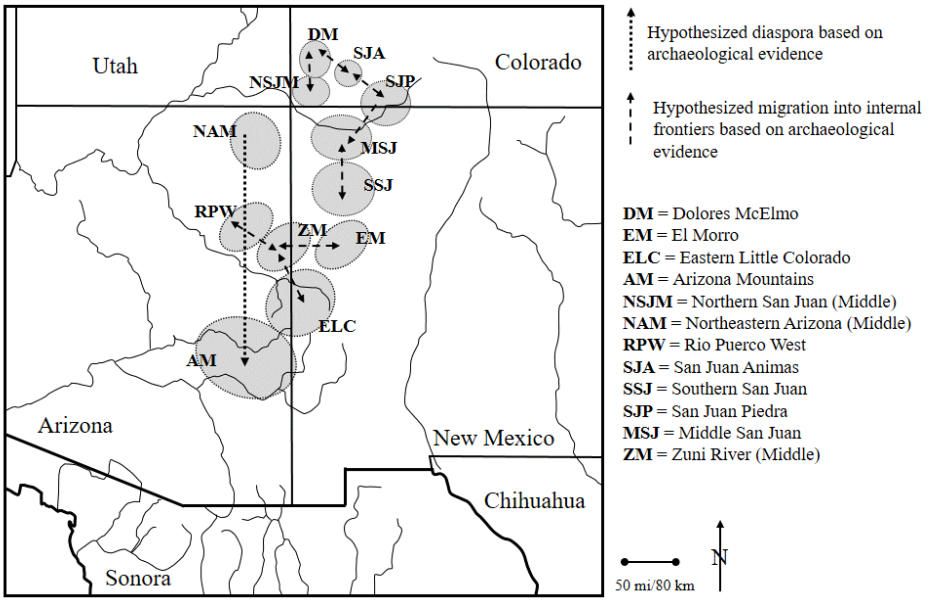

FIGURE 4: Late period (AD 1400–1700) reorganization

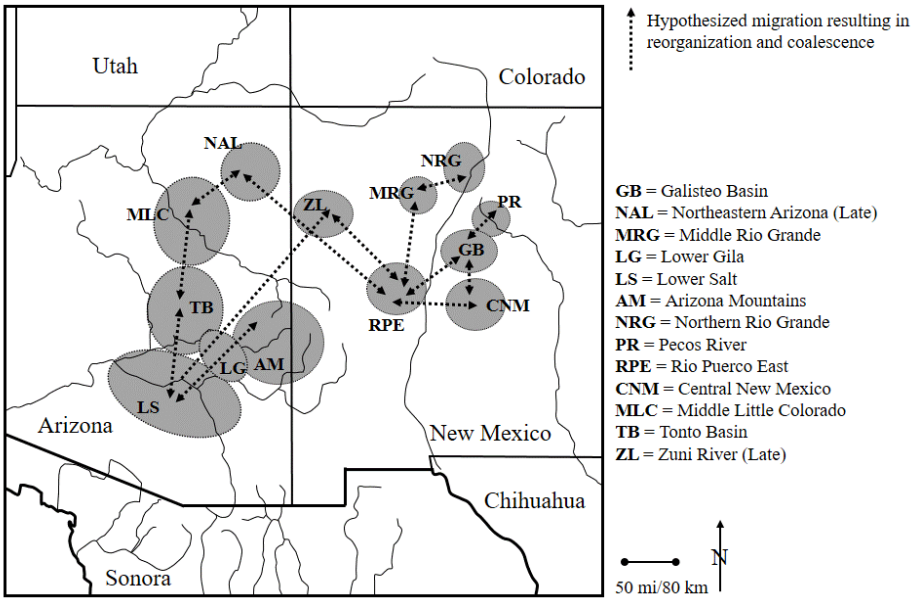

FIGURE 5: Principal Coordinates Analysis (PCA) testing Early period colonization of open landscapes

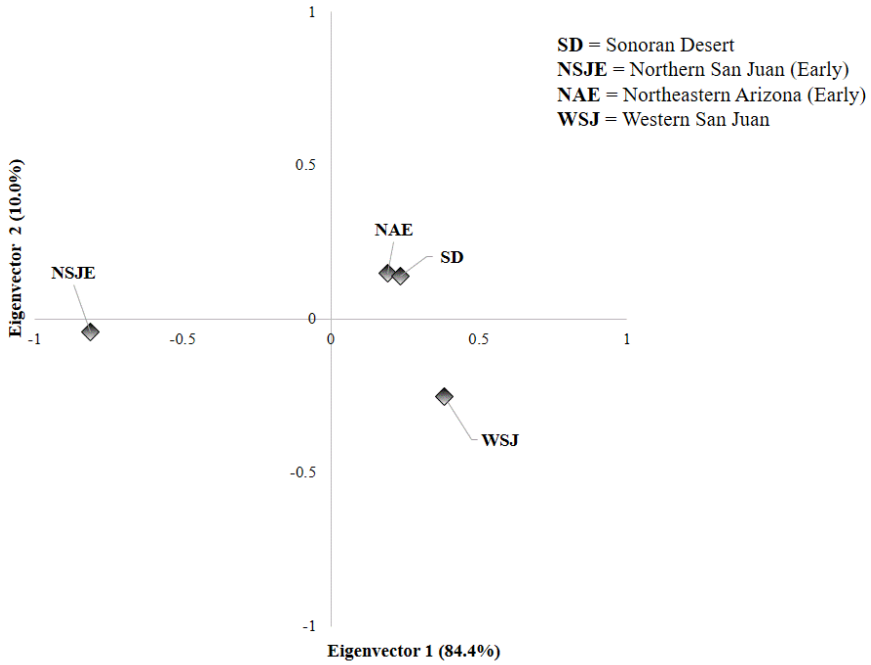

FIGURE 6: Principal Coordinates Analysis (PCA) of Middle Period migration into internal frontiers and diaspora

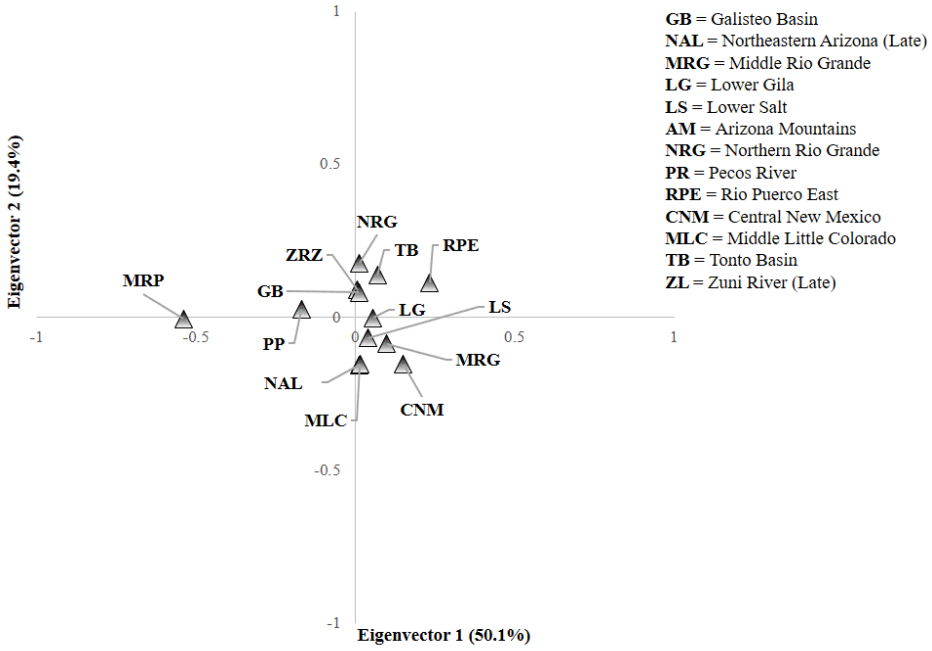

FIGURE 7: Principal Coordinates Analysis (PCA) of Late Period coalescence and reorganization

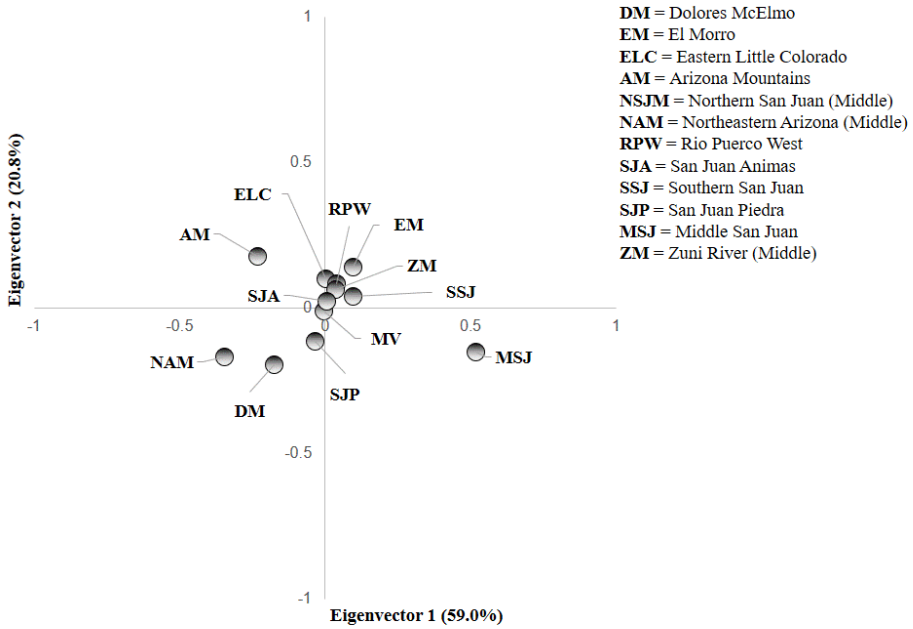

TABLE 1: Migration processes and expectations tested in this study

	Early Period (2100 BC-AD 500)	Middle Period (AD 700-1400)	Late Period (AD 1100-1696)
Colonization of Open Landscapes	High variance at origin locations due to gene flow; low variance at destination locations due to founder effect; affiliation between origin and destination locations	High variance at origin locations due to gene flow; low variance at destination locations due to founder effect; affiliation between origin and destination locations	High variance at origin locations due to gene flow; low variance at destination locations due to founder effect; affiliation between origin and destination locations
Migration into Internal Frontiers	No evidence for migration into internal frontiers	Low variance due to founder effect; affiliation with aggregated origin location	Low variance due to founder effect; affiliation with aggregated origin location
Large Scale Diaspora	No evidence of large scale diaspora expected	High variance at destination locations due to gene flow; affiliation between long distance origin and destination locations	High variance at destination locations due to gene flow; affiliation between long distance origin and destination locations
Coalescence and Reorganization	No evidence of coalescence and reorganization expected	High variance at destination locations due to gene flow; affiliation across region patterned by geographic distance	High variance at destination locations due to gene flow; affiliation across region patterned by geographic distance

TABLE 2: Samples Table

Temporal Period	Code	Sub-region	*n*	Date Range
Early	SD	Sonoran Desert	25	2100 BC–AD 50
	WSJ	Western San Juan	53	500 BC–AD 500
	NAE	Northeastern Arizona	8	500 BC–AD 500
	NSJE	Northern San Juan	11	500 BC–AD 500
Middle	SJA	San Juan Animas	20	AD 700–900
	NAM	Northeastern Arizona	27	AD 800–1300
	DM	Dolores McElmo	56	AD 850–1200
	SJP	San Juan Piedra	12	AD 850–1050
	SSJ	Southern San Juan	137	AD 920–1150
	ZM	Zuni River	8	AD 1000-1225
	RPW	Rio Puerco West	61	AD 1000-1275
	MSJ	Middle San Juan	51	AD 1020–1280
	ELC	Eastern Little Colorado	12	AD 1100–1300
	AZ	Arizona Mountains	116	AD 1200–1400
	NSJM	Northern San Juan	34	AD 1020–1280
	EM	El Morro	29	AD 1275–1375
Late	MLC	Middle Little Colorado	48	AD 1100–1450
	LS	Lower Salt River	113	AD 1150–1450
	LG	Lower Gila River	10	AD 1200–1400
	AM	Arizona Mountains	116	AD 1200–1400
	TB	Tonto Basin	20	AD 1200–1400
	PR	Pecos River	89	AD 1275–1400
	RPE	Rio Puerco East	24	AD 1300–1500
	MRG	Middle Rio Grande	38	AD 1325–1550
	NRG	Northern Rio Grande	76	AD 1325–1590
	NAL	Northeastern Arizona	8	AD 1325–1680
	GB	Galisteo Basin	71	AD 1250–1680
	ZL	Zuni River	70	AD 1380–1680
	CNM	Central New Mexico	72	AD 1400–1680

TABLE 3: Relethford-Blangero Analyses Results

Sub-region	Within-group phenotypic variance (unbiased) r(ii)	Observed	Expected	Residual	Standard error	p-value
WSJ	0.119	0.863	1.221	-0.358	0.129	0.589
NAE	0.062	0.454	1.300	**-0.846**	0.076	**>0.0001**
SD	0.654	1.567	1.295	**0.272**	0.723	**>0.0001**
NSJE	1.346	1.384	-0.479	**1.863**	1.895	**>0.0001**
EM	0.0174	0.4620	1.0620	-0.6000	0.0166	0.3277
ELC	0.0093	0.8120	1.0710	-0.2590	0.0312	0.9760
RPW	0.0366	0.3490	1.0410	**-0.6920**	0.0130	**0.0259**
ZM	0.0000	0.4710	1.0810	-0.6090	0.3216	1.0000
AM	0.0974	1.1250	0.9750	**0.1500**	0.0150	**0.0003**
NAM	0.1774	3.6660	0.8890	**2.7770**	0.0408	**0.0034**
SSJ	0.0630	0.8860	1.0120	**-0.1270**	0.0106	**0.0006**
MSJ	0.1583	0.6590	0.9090	**-0.2500**	0.0275	**0.0007**
DM	0.0447	1.5470	1.0320	0.5140	0.0200	0.0608
NSJM	0.0000	0.5110	1.0810	-0.5690	0.0039	1.0000
SJA	0.0599	0.6180	1.0160	-0.3980	0.0323	0.1059
SJP	0.0474	0.4790	1.0290	-0.5500	0.0413	0.2890
MLC	0.0293	0.5680	0.9060	-0.3370	0.0139	0.0721
CNM	0.0443	0.5750	0.8920	**-0.3170**	0.0128	**0.0107**
ZL	0.0699	0.7710	0.8680	**-0.0970**	0.0160	**0.0033**
LG	0.0000	0.5430	0.9330	-0.3900	0.0281	1.0000
LS	0.0104	0.7270	0.9230	-0.1960	0.0055	0.1005
MRG	0.0144	0.6170	0.9200	-0.3030	0.0130	0.3037
AM	0.1310	1.6630	0.8110	**0.8520**	0.0174	**0.0001**
NAL	0.0310	0.6100	0.9040	-0.2940	0.0521	0.5702
PP	0.2389	0.6020	0.7100	**-0.1080**	0.0252	**0.0001**
RPE	0.2777	1.3570	0.6740	**0.6830**	0.0537	**0.0013**
TB	0.1453	1.3030	0.7970	**0.5050**	0.0444	**0.0137**
GB	0.0882	1.4540	0.8510	**0.6040**	0.0176	**0.0016**
NRG	0.0562	0.8230	0.8810	**-0.0570**	0.0138	**0.0048**

SUPPLEMENTARY MATERIALS

SUPPLEMENTARY TABLE 1: Complete samples tables including sub-regions and archaeological sites included in this study

Code	Sub-region	*n*	Temporal Period	Date Range	Analysts
SD	**Sonoran Desert**	**25**	Early	2100 BC–AD 50	
	Las Capas	3			RB
	Wetlands	2			LLB
	Santa Cruz Bend	1			PM, LLB
	Los Pozos	1			ASM
	Donaldson	1			RB
	Stone Pipe	2			ASM
	La Playa	15			RB
WSJ	**Western San Juan**	**53**	Early	500 BC–AD 500	
	Grand Gulch, Cave 7	25			AH
	Grand Gulch, Cave 6	1			AH
	Grand Gulch, Cave 12	3			AH
	Grand Gulch, Cave 26	1			AH
	Grand Gulch, Cave 31	1			AH
	Grand Gulch, unknown	20			AH
	Glen Canyon, site 681	1			FS, AL
	Glen Canyon, Sand Dune Cave	1			FS, AL
NAE	**Northeastern Arizona**	**8**	Early	500 BC–AD 500	
	White Dog Cave	3			DMM
	Sayodneechee Cave	5			DMM
NSJE	**Northern San Juan**	**11**	Early	500 BC–AD 500	
	Falls Creek	5			DMM
	Tammarron	1			R&K
	Talus Village	4			DMM
	Ignacio Field Camp	1			F&W
SJA	**San Juan Animas**	**20**	Middle	AD 700–900	
	Crestview	2			DMM
	Bodo Canyon	3			DMM
	Ridges Basin	14			AS, DMM
	West Animas	1			DM
NAM	**Northeastern Arizona**	**27**	Middle	AD 800–1300	
	Black Mesa	19			RB
	Inscription House	4			EKR
	Keet Seel	2			EKR
	Kaibito Road	1			EKR
	Tsegi	1			EKR
DM	**Dolores McElmo**	**56**	Middle	AD 850–1200	
	Dolores Archaeological Project	12			AS
	Wallace Site	5			CJB
	Montezuma Canyon	5			MS

	Sand Canyon Pueblo	3			DM
	Lowry	8			BL
	Dominguez	1			LJS
	Ackmen	5			BL
	Castle Rock	3			DM
	5MT10010	2			PL
	5MT10207	1			MHD
	5MT10991	1			LS
	5MT7723	1			MHD
	5MT8899	1			KEB
	5MT8943	1			MHD
	5MT9924	2			PL
	5MT9934	3			SU
	5MT9943	2			PL
SJP	**San Juan Piedra**	**12**	Middle	AD 850–1050	
	LA4131	4			EKR
	LA4169	2			KB
	LA4195	4			KB
	LA4198	1			EKR
	LA4242	1			KB
SSJ	**Southern San Juan**	**137**	Middle	AD 920–1150	
	Pueblo del Arroyo	6			EKR, NJA
	Pueblo Bonito	62			AH; MS
	Fajada Butte	2			NJA
	Crownpoint	4			NJA
	Chaco Canyon	6			AH
	Chaco small sites	10			NJA
	Kin Kletso	2			EKR
	near Kin Ya'a	2			NJA
	BC sites	6			NJA
	Bc-59	7			EKR
	Bc-362	2			EKR
	9999	1			NJA
	9090	2			NJA
	2999	4			NJA
	1999	1			NJA
	1947	4			NJA
	1360	2			NJA
	721	1			NJA
	627	1			NJA
	577	1			NJA
	563	1			NJA
	397	1			NJA
	396	5			NJA
	299	4			NJA
ZM	**Zuni River**	**8**	Middle	AD 1000-1225	
	Village of the Great Kivas	8			MS
RPW	**Rio Puerco West**	**61**	Middle	AD 1000-1275	

	Whitewater Arroyo	2			CT
	Whitewater	18			TDS
	Petrified Forest	17			AH
	Manuelito	5			AH
	Kin Tiel	10			AH
	Allentown	9			JW
MSJ	**Middle San Juan**	**51**	Middle	AD 1020–1280	
	Aztec Pueblo	24			MS
	Tommy Site	7			MG
	Salmon Ruin	2			MG
	Mine Canyon Site	7			MG
	Lone Kiva Site	2			MG
	LA 65030	3			MS
	LA 37601	3			MS
	LA 37592	1			MS
	LA 37593	1			MS
	LA 3292	1			ER
ELC	**Eastern Little Colorado**	**12**	Middle	AD 1100-1300	
	Slade Ruin	5			RB
	Techado Spring	7			SP
NSJM	**Northern San Juan**	**34**	Middle	AD 1020–1280	
	Mug House	6			KB
	Big Juniper House	3			KB
	Badger House	3			KB
	Long House	5			KB
	Mesa Verde Museum	7			KB
	Site 1676	8			KB
	Site 1241	1			KB
	Site 1253	1			KB
EM	**El Morro**	**29**	Middle	AD 1275-1375	
	Heshotauthla	22			MS
	Pueblo de los Muertos	6			LS
	Atsinna	1			CT
MLC	**Middle Little Colorado**	**48**	Middle	AD 1100-1450	
	Wupatki	3			B&S
	Chaves Pass	32			AH
	Elden Pueblo	13			AH
LS	**Lower Salt**	**113**	Middle	AD 1150-1450	
	Las Acequias	3			PM
	Los Muertos	110			AH
LG	**Lower Gila**	**10**	Middle	AD 1200-1400	
	Togetzoge	10			MS
AM	**Arizona Mountains**	**116**	Middle	AD 1200-1400	
	Grasshopper Pueblo	53			RB
	Point of Pines Pueblo	22			RB
	W:10:52	9			TB
	Turkey Creek Pueblo	14			RB

	Kinishba	18			TB
TB	**Tonto Basin**	**20**	Middle	AD 1200-1400	
	AZ U:3:5	10			PM
	AZ U:3:405	4			PM
	AZ U:3:299	2			PM
	AZ U:3:298	1			PM
	AZ U:3:294	1			PM
	AZ U:4:33	1			PM
	AZ V:5:119	1			PM
PR	**Pecos River**	**89**	Middle	AD 1275-1400	
	Pecos Pueblo	89			EH
RPE	**Rio Puerco East**	**24**	Late	AD 1300-1500	
	Pottery Mound	24			MS
MRG	**Middle Rio Grande**	**38**	Late	AD 1325-1550	
	Kwasteyukwa	32			AH
	Jemez Valley	3			AH
	Guisiwa	3			AH
NRG	**Northern Rio Grande**	**76**	Late	AD 1325-1590	
	Puye	58			MS
	Otowi	10			AH
	Tsirege	8			AH
NAL	**Northeastern Arizona**	**8**	Late	AD 1325-1680	
	Awatobi	4			AH
	Homolovi	1			AH
	Sikyatki	3			AH
GB	**Galisteo Basin**	**71**	Late	AD 1250-1680	
	Arroyo Hondo	13			EO
	Pindi	13			MS
	Pueblo Largo	4			JW
	San Cristobal	41			MS
ZL	**Zuni River**	**70**	Late	AD 1380-1680	
	Hawikku	44			JW
	Old Zuni Church	26			EKR
CNM	**Central New Mexico**	**72**	Late	AD 1400-1680	
	Gran Quivira	64			MN
	Pueblo Pardo	8			MN

TABLE 2: List of analysts contributing data included in this study

Analyst Initials	Analyst Name
AH	Alan Hrdlicka
AL	Alexander Lindsay Jr.
AS	Ann Stodder
B&S	Baily and Schurr
BL	Brian Lesley
CB	Cindy Bradley
DMM	Dawn Mulhern
DM	Debra Martin
EO	Eric Ozolins
ER	Erik Reed
F&W	Fenga and Wendorf
FS	Floyd Sharrock
JW	James Watson
KB	Kenneth Bennet
LLB	Lorrie Lincoln-Babb
LS	Linda Smith
MD	Michael Dice
MG	Michelle Greene
MS	Michael Schillaci
NA	Nancy Akins
PL	Patricia Lambert
PM	Penny Minturn
R&W	Reed and Kainer
RB	Rachael Byrd
SU	Sally Underwood
TB	Theodora Burbank
TDS	T.D. Stewart

Supplementary Materials Table 3: Biodistance matrices (D^2) for each time period

	NAE	WSJ	SD	NSJE
NAE				1.4715
WSJ	0.1955 (0.0823)		0.2235	1.0800
SD	0.1807 (0.0875)	0.1051 (0.0374)		1.1607
NSJE	2.1658 (0.2941)	1.7051 (0.1845)	1.8034 (0.2076)	

	EM	ELC	RPW	ZM	AM	NAM	SSJ	MSJ	DM	NSJM	SJA	SJP
EM		0.0078	0.0097	0.0031	0.2084	0.2976	0.0054	0.3109	0.2209	0.0304	0.0417	0.0783
ELC	0.0005 (0.0401)		0.0313	0.0115	0.0852	0.2161	0.0409	0.3347	0.1129	0.0179	0.0151	0.0672
RPW	0.0115 (0.0208)	0.0399 (0.0454)		0.0329	0.1771	0.2397	0.0085	0.3397	0.1491	0.0247	0.0302	0.0695
ZM	0.0000 (0.0413)	0.0147 (0.0664)	0.0420 (0.0529)		0.1058	0.1946	0.0126	0.2839	0.1499	0.0025	0.0107	0.0090
AM	0.1467 (0.0413)	0.0579 (0.0472)	0.1548 (0.0317)	0.0761 (0.0602)		0.1931	0.2143	0.6784	0.1881	0.1263	0.1086	0.1817
NAM	0.2747 (0.0714)	0.2416 (0.0913)	0.2714 (0.0605)	0.2155 (0.1003)	0.1865 (0.0474)		0.2407	0.7754	0.0854	0.1432	0.1943	0.1056
SSJ	0.0199 (0.0196)	0.0684 (0.0528)	0.0186 (0.0129)	0.0412 (0.0496)	0.2473 (0.0315)	0.3300 (0.0599)		0.2569	0.1714	0.0243	0.0439	0.0561
MSJ	0.1699 (0.0495)	0.1990 (0.0770)	0.2126 (0.0437)	0.1534 (0.0814)	0.4247 (0.0543)	0.5857 (0.0894)	0.1533 (0.0321)		0.5133	0.3065	0.3068	0.3334
DM	0.1207 (0.0473)	0.0738 (0.0580)	0.1134 (0.0379)	0.1016 (0.0735)	0.1285 (0.0364)	0.0994 (0.0450)	0.1843 (0.0413)	0.2805 (0.0587)		0.0859	0.0902	0.0546
NSJM	0.0163 (0.0212)	0.0210 (0.0393)	0.0322 (0.0187)	0.0027 (0.0373)	0.0965 (0.0259)	0.1578 (0.0478)	0.0624 (0.0202)	0.1705 (0.0399)	0.0476 (0.0269)		0.0020	0.0099
SJA	0.0814 (0.0500)	0.0692 (0.0655)	0.0768 (0.0420)	0.0689 (0.0732)	0.0929 (0.0421)	0.3073 (0.0851)	0.1735 (0.0529)	0.2371 (0.0673)	0.1059 (0.0526)	0.0443 (0.0348)		0.0273
SJP	0.1004 (0.0657)	0.1363 (0.0917)	0.1279 (0.0638)	0.0318 (0.0724)	0.1962 (0.0723)	0.0967 (0.0659)	0.1475 (0.0634)	0.2379 (0.0827)	0.0377 (0.0494)	0.0354 (0.0434)	0.1175 (0.0761)	

	MLC	CNM	ZL	LG	LS	MRG	AM	NAL	PR	RPE	TB	GB	NRG
MLC		0.0385	0.0891	0.0064	0.0151	0.0705	0.3257	0.0000	0.0976	0.1208	0.1543	0.0679	0.1062
CNM	0.0259 (0.0187)		0.1038	0.0213	0.0573	0.1149	0.5226	0.0401	0.1829	0.1261	0.1838	0.0865	0.1469
ZL	0.1758 (0.0397)	0.1233 (0.0299)		0.0193	0.0299	0.1035	0.3401	0.0905	0.0649	0.1016	0.1111	0.0126	0.0349
LG	0.0100 (0.0391)	0.0000 (0.0322)	0.0496 (0.0490)		0.0000	0.1026	0.3444	0.0013	0.0902	0.0447	0.0689	0.0142	0.0236
LS	0.0199 (0.0154)	0.0382 (0.0161)	0.0606 (0.0197)	0.0000 (0.0286)		0.0719	0.3573	0.0107	0.0833	0.0869	0.1557	0.0395	0.0654
MRG	0.0452 (0.0274)	0.0583 (0.0270)	0.1041 (0.0342)	0.0502 (0.0534)	0.0279 (0.0193)		0.4787	0.0602	0.1259	0.1271	0.1465	0.0835	0.1576
AM	0.1823 (0.0373)	0.2728 (0.0393)	0.2312 (0.0367)	0.1849 (0.0754)	0.1752 (0.0281)	0.2000 (0.0426)		0.3276	0.1905	0.6222	0.4573	0.3325	0.3478
NAL	0.0000 (0.0302)	0.0258 (0.0554)	0.2109 (0.0932)	0.0082 (0.0739)	0.0187 (0.0515)	0.0434 (0.0646)	0.1967 (0.0908)		0.0905	0.1329	0.1102	0.0718	0.1213
PR	0.3421 (0.0516)	0.3982 (0.0489)	0.2552 (0.0398)	0.3437 (0.0994)	0.2782 (0.0366)	0.2828 (0.5124)	0.1609 (0.0288)	0.3556 (0.1157)		0.2274	0.1748	0.0443	0.0887
RPE	0.3210 (0.0714)	0.2722 (0.0622)	0.2858 (0.0630)	0.1701 (0.0859)	0.2546 (0.0573)	0.2759 (0.0699)	0.6953 (0.0926)	0.1326 (0.1326)	0.8145 (0.1016)		0.1427	0.0804	0.5273
TB	0.2398 (0.6723)	0.2138 (0.0603)	0.1916 (0.0577)	0.1071 (0.0760)	0.2030 (0.0563)	0.1621 (0.0595)	0.3468 (0.0721)	0.1827 (0.1047)	0.4652 (0.0839)	0.3248 (0.0887)		0.0973	0.1133
GB	0.1985 (0.0418)	0.1343 (0.0310)	0.0379 (0.0185)	0.0756 (0.0555)	0.1073 (0.0251)	0.1202 (0.0363)	0.2671 (0.0391)	0.2497 (0.1015)	0.2067 (0.0359)	0.2415 (0.0590)	0.1927 (0.0578)		0.0209
NRG	0.1381 (0.0349)	0.1289 (0.0299)	0.0546 (0.0209)	0.0230 (0.0408)	0.0679 (0.0201)	0.1055 (0.0339)	0.2009 (0.0335)	0.1857 (0.0903)	0.2701 (0.0399)	0.1666 (0.0497)	0.1633 (0.0534)	0.0366 (0.078)	

APPENDIX C

Integrating Biological Affiliation Evidence into the Cultural Affiliation Process in the Southwest

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Abstract

The primary goal of this study was to develop a tool to estimate biological affiliation in archaeological human skeletal remains from sites in the North American Southwest to strengthen integration of biological evidence within the cultural affiliation process. This "Arizona Biological Affiliation Database" (AzBAD) is composed of data on cranial morphometrics from eleven geographically and temporally defined groups represented by 1,841individuals from the region. The data were imported as a custom database into the commonly used forensic classification software, Fordisc 3.1. Here, we present the reasoning for, and composition of this tool, along with a methodological approach for its use by testing a case study to illustrate its applicability in the cultural affiliation process for repatriation purposes according to state and federal mandates. The test case focuses on a cranium donated to the Arizona State Museum (ASM) in 1967 with limited associated contextual information beyond the cultural designation of "Late Classic Period Hohokam." Facial morphometrics from the cranium was tested against the reference groups in the AzBAD using linear discriminant function, Mahalanobis distance, and leave-one-out-cross-validation analyses along with posterior and typicality probabilities to calculate the closest biological affiliation. Results indicate a close biological affiliation with the Northeastern Arizona/Zuni River (AD 1300–1700) reference group. The discordance between assumed association and estimated affiliation serve to highlight how population histories are complicated by past episodes of migration and gene flow in the region. This research demonstrates that appropriate reference group samples and explicitly addressed assumptions for biological evidence can contribute an important perspective to cultural affiliation determinations and facilitate the repatriation processes.

One of the primary impediments to determining cultural affiliation for facilitating repatriation to descendant communities is a lack of contextual information. Just a few examples include, poor or missing documentation, non-diagnostic associated artifacts, contradictory information from oral traditions, or limited information about population histories in the region. Establishing lineal descent could arguably be the most direct biological mechanism to facilitate cultural affiliation but this often impossible when dealing with prehispanic archaeological remains. Increasingly, more high-resolution mtDNA studies conducted in the Southwest shed light on ancestral haplogroup frequencies and group-relatedness through maternal lineages (Kennett et al. 2017; Malhi et al. 2003; Morales-Arce et al. 2017; Snow et al. 2010; 2011). However, these studies are limited due to lack of preservation and access, and the ethical concerns of descendant communities (Schroeder et al. 2006).

As an alternative to destructive approaches, comparisons of skeletal morphology are commonly used by bioarchaeologists to assist in estimating biological relatedness and affiliation. However, evaluating skeletal morphology of human remains with limited associated contextual information can only be effective if appropriate reference groups are available. This study expands on the morphological approach by developing a comparative cranial morphometric database, representing over 3,500 years of occupation across the North American Southwest (Southwest), as a reference tool for assessing biological affiliation of unidentified human remains or human remains lacking precise depositional contextual information. Understanding the connections between present and past populations, including biological ones, is of interest both descendant communities and anthropologists, and using non-destructive methods can help balance the needs and rights of these groups. Here we propose a process for integrating cranial

morphometric indicators as biological evidence in the cultural affiliation determination process, as mandated under state and federal legislative repatriation mandates.

Cultural Affiliation Criteria and Biological Evidence

Passed in 1990, the Native American Graves Protection and Repatriation Act (NAGPRA) (25 USC 3001-3013) mandates that federal agencies and institutions receiving federal funds or curating human remains found on federal or tribal land must follow a process for documenting and transferring the remains to lineal descendants, or those with established cultural affiliation with an identifiable earlier group. Cultural affiliation (25 U.S.C. 3001(2)) is defined as a "relationship of shared group identity which can be reasonably traced historically or prehistorically between a present-day Indian tribe or Native Hawaiian organization (NHO) and an identifiable earlier group." A preponderance of eleven lines of evidence is needed for this determination, including: 1) geographical, 2) kinship, 3) biological, 4) archaeological, 5) anthropological, 6) linguistic, 7) folklore, 8) oral tradition, 9) historical evidence, or 10) other information or 11) expert opinion (43 C.F.R 10.2(2e)). Museums or federal agencies that have control of Native American human remains and other cultural items are responsible for determining cultural affiliation.

The U.S. Department of the Interior released three criteria for determining cultural affiliation (https://www.nps.gov/nagpra/TRAINING/Cultural_Affiliation.pdf); the first being the existence of a federally recognized tribe or NHO. The second and third criteria involve the requirement of evidence for the existence of an identifiable earlier group by, 1) establishing the identity and cultural characteristics of the earlier group, 2) documenting distinct patterns or material cultural manufacture and distribution methods of the earlier group, and 3) establishing

the existence of the earlier group as a biologically distinct population. Further information is not provided as to the definition of a 'biologically distinct population'. The third and final criterion provided for determining cultural affiliation relies on evidence of a shared group identity that can be traced between the earlier group and the present-day tribe or NHO. Specifically, evidence must establish that the present day group has been identified as descending from the earlier group (43 C.F.R. 10.14).

Biological evidence is needed to establish an earlier group as a biologically distinct population, as well as to identify that a present day tribe descended from the earlier group. Aspects of biological group identity, in particular biological relatedness and affiliation, must be considered within the cultural affiliation process. Biological group identity, like social group identity, is notoriously dynamic, multi-scalar, and is continually shared and altered (Beisaw 2010; Dongoske et al. 1997). Cameron and Ortman (2017) argue that by linking ancient human remains and their objects with specific descendant groups forces Native Americans to project their current identity to the past. Not only does this ignore complex socio-cultural, biological, and historical processes integrated in the development of shared group identity, but it is evolutionarily misleading (Schillaci and Bustard 2010). Furthermore, the requisite determination of an earlier identifiable group through distinctive material cultural manufacture, distribution methods, and as a biologically distinct population misconstrues archaeological cultures and present-day tribes as homogenous, distinctive entities with a common origin.

If the totality of information, including consultation with tribes, does not allow for establishing a relationship of shared group identity, the remains are deemed culturally unidentifiable. Culturally unidentifiable human remains are defined as human remains in museum or Federal agency collections for which no lineal descent or culturally affiliated Indian

tribe or NHO has been identified through the inventory process (43 CFR 10.2 (e) (2)). In 2010, the United States (US) Department of the Interior published regulations for the disposition of these unidentifiable human remains (43 CFR 10.11). This rule mandates museums to re-consider their original inventories and work to determine if the remains were recovered from tribal or aboriginal land (Colwell-Chanthaphonh et al. 2011). Priority of control of culturally unidentifiable remains is given first to the tribe that owns the tribal lands from which the remains were removed, then the tribes from whose aboriginal lands the remains were removed. The regulations require that museums produce an inventory of culturally unidentifiable remains with associated geographic data, consult with tribes with 90 days of a claim, publish Notices of Inventory Completion regardless of lack of evidence, and transfer remains that were recovered from tribal or aboriginal land (Colwell-Chanthaphonh et al. 2011). However, if the remains are from an unknown location and are unaffiliated, the museum is to continue holding these remains until a new rule is promulgated (43 CFR 10.15(b)).

Human Remains on State and Private Land in Arizona

Remains in collections and discovered on tribal and federal lands are covered by NAGPRA, whereas state law covers new discoveries of human remains. State-level legislation and restrictions imposed regarding archaeological investigations of human skeletal remains and their contexts range from relatively loose, such as in New York, to very strict, such as those in Iowa (Arnold and Jeske 2014). In Arizona, the Arizona Antiquities Act, Arizona Revised Statues (ARS) 41-841 et seq. provides protection against the removal of archaeological artifacts from land owned or controlled by the State of Arizona without a permit issued by the Director of the Arizona State Museum (ASM). ARS §41-844 was issued in 1990 and mandated that a person in

charge of any excavations on state land must report any archaeological, paleontological, or historical site (>50 years old) to the ASM Director. If human remains, funerary objects, sacred ceremonial objects or objects of national or tribal patrimony are discovered, five stakeholders are notified including: 1) individuals that may have a direct kinship relationship to the human remains, 2) all groups reasonably believed to have cultural or religious affinity to the remains or objects, 3) appropriate members of the ASM curatorial staff, 4) faculty members of the state universities who have significant scholarly interest in the remains, and 5) the State Historic Preservation Office (SHPO). In addition, notice is given to the tribes that occupy or have occupied the land on which the discovery is made, to the Governor's Office on Tribal Relations,, and the Intertribal Council of Arizona. Further consultation than ensues.

In addition, ARS. §41-865) requires that human remains older than 50 years of age and funerary objects discovered on private land must be reported by landowners or their designated agents to the Director of ASM. Groups with cultural affinity have claimant's rights. This legislation also lists guidelines for reporting, recovery, and repatriation procedures and states that there will be legal punishment for individuals who possess, sell, or transfer human remains. Both ARS § 41-844 and § 41-865 broadly define "cultural affinity" a relationship which can be reasonably traced historically or prehistorically between a present claimant and an identifiable earlier group. Establishing cultural affinity in the state statutes differs from cultural affiliation as defined in the federal law in that it does not require the determination of a shared group identity; however, both can integrate biological evidence to identify such connections.

Study Purpose and Intent

The primary goal of this project is to develop a tool to estimate biological affiliation in archaeological human skeletal remains to more effectively integrate biological evidence into the cultural affinity and cultural affiliation determination processes in Arizona specifically, and across the Southwest region more broadly. Here we describe the "Arizona Biological Affiliation Database" (AzBAD) which is composed of geographically and temporally distinguished data on cranial morphometrics from across the region. Cranial morphology is moderately heritable and reflects neutral genetic variation in human populations (see Betti et al. 2009; Carson 2006; Manica et al. 2007; Smith 2011; von Cramon Taubadel 2009; Zichello 2018). We recommend a process for assessing cranial morphology from human remains with limited or no contextual information—what often might be classified as culturally unidentifiable under NAGPRA—to estimate biological affiliation between to known archaeological skeletal samples within the SW reference database. We identify the statistical assumptions associated with this process as outlined by the developers of Fordisc, a widely-used forensic software. Finally, we test the utility of the database and its associated approach with a case study. This customized database will strengthen the use of biological evidence across the SW region by providing the most comprehensive, representative reference groups available to date.

III. Materials and Methods

Standard craniofacial measurements and sex assessment based on os coxae osteological indicators were collected by the authors and compiled with previously published data from a total of 1,841 (927 females, 877 males; 37 unidentified) prehistoric and historic adult (18+ years of age) individuals excavated from archaeological sites in the Southwest. Eleven reference

groups designated by geographic area and broad temporal period were formed (Table 1; Figure 1). These geographic areas are defined by river and tributary drainages, including the Little Colorado, Lower Salt/Lower Gila, Northern and Middle Rio Grande, Northern and Southern San Juan, Central Arizona/Tonto Basin, and Northeastern Arizona/Zuni River. Other areas are defined by landforms including the Arizona Mountains/Mogollon Highlands and Sonoran Desert which recognize their distinctive climate and elevation. The Southeastern Utah/Northeastern Utah is the only geographic area that is defined by state political boundaries. A complete list of sites and numbers of individuals included in each geographic area is included in the Supplementary Materials: Table 1. These reference groups are represented by bounded geographic areas that serve to group crania in this study. This is done primarily to address statistical needs of creating comparative discrete groups (Figure 1). Additionally, it is also important to note that not all areas of the Southwest are included in the initial version of the Southwest dataset due to the lack of accessibility and preservation of adequate numbers of human skeletal remains during data collection. Groups were then categorized in broad temporal groups, including Early (2100 BC–AD 500), Middle (500 BC–AD 1300), Middle (AD 900–1400), Middle-Late (AD 1300–1700). These groups represent substantial time depth, namely the Early (2,500 years) and Early-Middle (1,800 years) groups, separating the individuals in this way allows for comparing biological affiliation of groups with a basic level of temporal control while maintaining large sample sizes required for multivariate analysis. Altogether, the reference samples included span 3,800 years of occupation in the Southwest US.

It is important to acknowledge that not all geographic areas in Arizona, and much less the entire North American Southwest, are represented in the biological affiliation database. Many past groups living in northcentral and northwestern Arizona, near the Grand Canyon, as in

western Arizona including the Hualapai, Paiute (Kaibab, Moapa), Chemehuevi are not well represented, so it is impossible to say at this time if meaningful relationships can be elucidated.

One individual with cranial morphometric data and limited contextual data archived at Arizona State Museum provided the opportunity to assess biological affiliation against the comparative reference groups. This individual was an adult male with minimal associated contextual information. The only information on file was a description that the remains were found at "the old Amarisca Ranch," presumably located in southern Arizona based on details provided in a 1967 letter addressed to a Norton Allen, a well-known avocational salvage archaeologist (Ferg 2010; Ferg and Schwartzlose 2008) from Emil C. Haury. Haury notes:

> there is nothing specifically definitive about it (the cranium), but I suppose we have to take the position that by the 13th or 14th centuries things had gotten pretty well mixed if any of our Southwestern groups ever did have some outstanding identifying features.

Kenneth Bennett, one of Haury's graduate students, drafted a report that included the collection of standardized cranial measurements of the individual. The individual was described as a Late Classic Period Hohokam adult male individual (AD 1300–1450) 25–35 years of age at death, with post-cranial remains cremated, however a small portion of the cranium only moderately burned. Bennett states:

> metrically the skull of this individual is well within the range given for the large Western Pueblo population at Point of Pines, Arizona, which during the later occupation was in large part contemporaneous with the Late Classic Period Hohokam.

We hypothesize that, if Bennett's inferences are correct and the reference groups are appropriately structured and tested, this individual will classify with high probability within the Lower Salt/Lower Gila reference group.

IV. Methods

Measurement collection and selection for analysis

The construction of the database began with the manual collection of 34 standardized cranial and mandibular measurements by the authors following descriptions listed in Buikstra and Ubelaker (1994: 74–78). We collected measurements from human remains excavated from the Sonoran Desert, Central Arizona, Arizona Mountains/Mogollon Highlands, Little Colorado, Southeastern Utah/Northeastern Arizona, and Northern San Juan geographic areas. Individuals from archaeological sites located in geographic areas in Arizona, comprise the Arizona Biological Affiliation Database (AzBAD). Additional data from all other geographic areas were provided by other biological anthropologists and archaeologists working in the region, and compiled from published reports, dissertations, and archival documents (see Table 1: Supplementary Materials for sources).

Of the original cranial measurements collected, 15 facial measurements were identified and selected to be included in the initial analysis but, as following sections address, only eight of these measurements were ultimately used in the biological affiliation analysis (Table 2; Figure 2). Facial measurements were exclusively chosen to avoid the effects of cranial modification due to localized pressure from cradle boarding, which primarily affects occipital and parietal bone shape in many SW populations (Droessler 1981; Kohn et al. 1995).

Because the morphometric measurements included in the database were collected by multiple analysts, inter-observer error becomes an obstacle confronting the reliability of the reference group database to classify individuals accurately. Cranial measurements reported in the first half of the 20th century, such as those collected by early physical anthropologists Earnest Hooton and Ales Hrdlička, have somewhat variable descriptions that have since been

standardized (see Bass 1971; Buikstra and Ubelaker 1994; Howells 1973; Martin 1956; Moore-Jansen et al. 1994). Stojanowski and Euber (2011) examined consistency in measurement protocol throughout Hrdlička's *Catalog* series, and against Howells (1973, 1989) measurement descriptions and found that most of Hrdlička's measurements did not strictly align with those of Howell's, which are generally cited as the current protocol for collecting linear cranial measurements (see Buikstra and Ubelaker 1994). Orbital breadth, orbital height, and nasal height are not consistently defined by Hrdlička throughout the *Catalog* series, and they recommend working with caution when including these variables (Stojanowski and Euber 2011). Ortman (2010) reports that systematic inter-observer error was encountered for orbital breadth and interorbital breadth measurements, because the landmarks used for these measurements in Howells (1973) and Buikstra and Ubelaker (1994) are different and then standardizes to the Howells measurements. However, when Ortman (2012) looked at the same measurements that were collected by the same individuals (Schillaci and Hrdlička) and (Schillaci and Reed) linear regression analyses demonstrated high correlation with standard errors ranging from 1.08mm for paired measurements by Schillaci and Reed, and 1.28mm for paired measurements by Schillaci and Hrdlička. This suggests that measurements recorded by these three analysts, even if descriptions of measurements varied in language, likely do not vary more than a few millimeters at most. Although not directly tested here, the effect these small differences are potentially numerous and yet often unavoidable when working with and comparing bioarchaeological data when the remains themselves are no longer accessible.

Data preparation and Fordisc 3.1

Fordisc 3.1 is a computer program commonly used by forensic anthropologists to reconstruct ancestry by classifying adults into known reference groups using standard cranial measurements (Jantz and Ousley 2005; 2012; Ousley and Jantz 2012). Howell's (1973) international dataset, including 28 reference groups of known ancestry, is often used in studies involving comparison with individuals from the 19th century. Also included in Fordisc is the Forensic Data Bank (FDB) which comprises 13 samples of individuals born after 1930, yet also include people from the 19th century Terry and Hamann-Todd collections. These reference samples are most appropriate for historic and modern case comparison and for use with individuals born from the 20th century onward. Neither of these historic and modern cranial morphometric databases currently available in Fordisc is applicable for earlier individuals from archaeological sites. One option Fordisc contains is to input data to create a custom database which we utilize in this study. All cranial morphometric and associated categorical data were thus formatted following the software manual guidelines and uploaded into the Fordisc software.

Before beginning analyses, outliers were removed by graphically identifying individuals far from the group centroids using Fordisc's built-in canonical scatterplots with all reference groups. Additionally, confidence ellipses are set to enclose an area including all the variation in each reference group and help visualize reference group variation and dispersion. Groups that are less affected by differences in variance are more circular and elongated ellipses signify non-circular variation around means (Kovarovic et al. 2011). By visually assessing and comparing ellipse shape around each reference group an initial impression of group variation similarity can be gained. If the level of variation is roughly the same among reference groups, it is expected that confidence ellipses will be similar in size, shape, and orientation.

IV. Analysis

Linear Discriminant Function Analysis

Fordisc 3.1 utilizes Discriminant Function analyses that involve classification of an unknown specimen into reference groups of known membership. With Linear Discriminant Function Analysis (LDFA), a factor (or numerical weight) is calculated for each measurement or observation that, when summed, maximizes mean differences among groups. The discriminant function score of the unknown individual is compared to the centroid for each reference group. The unknown individual is classified into the most similar multivariate group, which is the one to with which it has the smallest Mahalanobis distances (D^2) (Mahalanobis 1936; Ousley and Jantz 2012). Mahalanobis distances are the outcome of a multivariate assessment of population sample difference that takes into account variance and covariance. Groups cluster around the mean discriminant scores, or centroids, and classification is based on each case's proximity to the centroids. These types of multivariate analyses operate under a series of assumptions that, if met, result in optimal statistical outcome.

Assumptions

The number of groups, number of predictor variables, and sample size of each group affect accuracy rates, and along with three main assumptions, must be addressed in order to appropriately run an LDFA. These assumptions apply to reference group samples and include: 1) sufficiently large and representative sample sizes, 2) multivariate normal distribution, and 3) relatively similar levels of variance (Ousley and Jantz 2012). Having sufficiently large and representative reference group samples represented by a statistically appropriate number of measurements is critically important to LDFA. In some situations common to taxonomic and

archaeological analyses reducing the number of measurements is necessary if working with relatively small sample sizes (Marcus 1990). One main point of contention in using the Fordisc software is how the results play out even in the source population in which the unknown case is tested against is not present. The second point of contention is the number of variables used in the analysis; some argue that more variables increase accuracy (Elliot and Collard 2009; Hubbe and Neves 2007) and others state that using too many variables reduces reliability and can inaccurately inflate the 'fit' (i.e., over-fit) of an unknown individual with reference groups (Jantz and Ousley 2005). Developers argue that the software's poor performance is largely human implementation error and misinterpretation of the results (Fried et al. 2005)

Others argue that accurate cranial morphometric analyses require upwards of 50 cranial measurements such as those present in the Howells database (Hubbe and Neves 2007; Kovarovic et al. 2011; Strauss and Hubbe 2010). Kovarovic and colleagues (2011) suggest that unequal sample size across groups and small samples are likely to increase over-fit and reduce generalizability of results. Large samples should be used when possible, but size heterogeneity may have consequences on the estimate of the random chance baseline. We follow the recommendation of Fordisc developers regarding reference group sample size being three-times the number of measurements included in each analysis, but not so large to avoid over-fitting (Huberty 1994; Jantz and Ousley 2005; Ousley and Jantz 2012). It is important to consider the classification rate to the total number of reference groups as well. For example, 50% classification accuracy for 10 groups is relatively good compared to that with only two groups.

The second and third assumptions of LDFA are that skeletal measurements are more or less normally distributed, and that reference groups have relatively equal within-group variance-covariance matrices. This assumption is often violated in taxonomic and archaeological

applications (Ousley and Jantz 2012). Fordisc has a built-in analysis that provides a *p*-value for a test of equal within-group variability (a.k.a., [VCVM] homogeneity test Chi-square) (Legendre and Legendre 1998). Leave-one-out-cross-validation (LOOCV) is helpful for estimating error rates of discriminant functions and for revealing over-fitting (using too many measurements for group sizes) (Huberty 1994). Kovarovic et al. (2011) argue that is very important to address over-fitting when using LDFA through cross validation, and to assess the probability of correctly classifying cases by chance. Cross-validation is chosen as well as stepwise selection to calculate variance-covariance matrices with jackknife (n-1 and rerun) analyses to help identify outliers and provide additional statistics on sample composition. When all individuals have been classified in this way, the total number of correctly classified individuals is the expected classification accuracy. This analysis avoids the bias of a lower estimated rate inherent when a reference group is tested against all reference groups in one of which the individual is a member.

Posterior Probabilities (PP)

Probabilities that the unknown individual comes from each reference group under the assumption that it actually belongs to one of the reference groups are called posterior probabilities. They are derived from Mahalanobis distances, can be weighted, and are generally standardized (Kovarovic et al. 2011). A higher posterior probability (>0.9) indicates the unidentified individual is more similar to that group compared with the others and more likely to be a correct classification than a lower posterior probability (<0.7). Additionally if posterior probabilities are spread out evenly among the reference groups for an individual, there is less confidence in the accuracy of the classification so this must also be examined.

Typicality Probabilities (TP)

Probabilities of the likelihood that an unknown individual belongs to each reference groups are called typicality probabilities. These help indicate if an unknown could belong to several reference groups or none of the reference groups, and are calculated based on the average variability of all groups in the analysis using absolute rather than relative distances. Typicality probabilities are calculated in three ways using Fordisc, including F, Chi, and R. Type F that provide the probability based on the F distribution, Chi-square distribution, and ranked probability, respectively. Typicality probabilities are not standardized, and are an estimate if a case is an outlier. When a case is extremely distant from the closest group, it is unlikely to belong to any of the groups included in the analysis (Kovarovic et al. 2011). Typicality probabilities that are below 0.05 for a group (such as with a p-value for statistical significance) should be viewed skeptically and measurement error should be inferred (Ousley and Jantz 2012). If TP's are low for each group, that the posterior probabilities (and thus, the entire classification) should not be accurate with a likelihood that the unknown individual does not belong to any of the reference groups.

V. Results

The biological affiliation analysis of the test individual began with the initial run of the LDFA analysis that included all 11 of the reference groups. Geographic area, sex, and measurements were coded, and measurements were labeled with Howells (1973) measurement abbreviations. From this, nine outliers were identified and removed as they were extremely divergent and dramatically skewed sample variation. The LDFA was then re-run without the outliers. The test individual classified into Group 6 (Lower Salt/Lower Gila) as results indicated

the smallest Mahalanobis distance and largest posterior probability. However, a very low LOOCV percentage (25.8%) indicated very low classification accuracy, and thus low validity. This was due to Groups 5, 6, 7 being without any correct classifications, or a 0% classification rate. So, although the initial results appear to meet expectations, that the test individual has a closer biological affiliation with the Lower Salt/Lower Gila reference group, since three groups did not receive any correct classifications they were removed, and the analysis was re-run without these groups to see if LOOCV percentages would be improved. The LDFA was subsequently run two additional times, each time removing reference groups with very low LOOCV percentage.

In the second analysis, the test individual classified with Group 11 (Northeastern Arizona/Zuni River), which had the smallest distance to the centroid and highest probability. Four groups, including group 2, 3, 9, and 10 have cross-validation correct percentages under 30%, and thus were removed for the final LDFA run. The final LDFA analysis includes Group 1 (Sonoran Desert), Group 4 (Middle/Southern San Juan), Group 8 (Arizona Mountains/Mogollon Highlands) and Group 11 (Northeastern Arizona/Zuni River) with a LOOCV correct percentage of 69.2%. The test individual was most similar to Group 11. Mahalanobis distances, Posterior and Typicality Probabilities, and percentage of correct classifications are presented in Table 3. Posterior probabilities indicate the closest affiliation of the test individual with reference group 11 (PP = 0.709), and with TP's estimating between 0.658-0.706, signifying the likelihood (66-71%) the test individual belongs to the reference group based on total variability among all of the reference groups included in the analysis. These results demonstrate a relatively high classification accuracy that is much better than random (compared with the equal prior probability of 25%). Canonical Variate Analysis (Figure 3) visually demonstrates reference

group variance and the relative position of the test individual within morphometric space. Centroids for each reference group are shown by the number code given to each group. The test individual is clearly positioned closest to the group 11 centroid.

The natural log of the determinant, which is the overall variance minus the overall covariance represents the total amount of variation is 16.3168. Since it is much greater than 0, this means that there is enough variation to provide the best matrix calculations (Ousley and Jantz 2012). VCVM homogeneity test (Kullback ChiSq) (94.32 with 108 df; $p = 0.82$) is a test for equal within group variability. In this case we fail to reject the null hypothesis that each group's VCM is the same, there is no indication in the results that the reference groups included in the final analysis differ significantly. Therefore, the third assumption of reference group homogeneity is met.

Biological Affiliation and the Arizona Government-to-Government Consultation Toolkit

Given the successful application of AzBAD to estimate biological affiliation with an unprovenienced individual, the next question is: How can we use this information to contribute to establishing cultural affiliation or affinity and work toward consultation and repatriation? In Arizona, the Arizona State Historic Preservation Office (SHPO) and Salt River Pima-Maricopa Indian Community (SRP-MIC) partnered to create a Government to Government (G2G) Consultation Toolkit (https://sites.google.com/view/az-consultation-toolkit/home) designed to facilitate the consultation process and help tribes and agencies meet the requirements of the National Historic Preservation Act , the State Historic Preservation Act, and other state and federal statutes. This toolkit includes a consultation map that allows for the user to click on the area of discovery and learn the claimant tribes for the sub-region and is useful for recognized

which tribes are requesting to be contacted and consulted with based on the location of ancestral skeletal remains.

One potential use for the G2G Toolkit would be in conjunction with biological affiliation information (Table 4). Using the classification information provided in the analysis here, the test individual classified into reference group 11, Northeastern Arizona and Zuni River. Table 4 offers suggested tribes with whom to consult on cultural affiliation based on biological affiliation evidence. Since the reference groups are tied to specific geographic areas this is a helpful method for using the information provided to support more engaged work with descendant communities.

VI. Discussion

The Arizona Biological Affiliation Database shows potential as a population reference tool to be used in connecting unidentified, unaffiliated, and unprovenienced individuals with known archaeological samples, demonstrating morphological aspects of shared biological affinity. This database will allow for a more consistent application of morphological affiliation as biological evidence in cultural affiliation determination across the Southwest and serves as a model for how to apply databases with similar goals within other regions, or perhaps in international contexts.

Analysts using this approach must be aware of the population histories, specifically migration patterns, representing each reference group as they directly impact cranial morphological variation and affiliation. Although the test individual included in this study did not meet initial biological affiliation expectations of being most closely related to individuals excavated from the Lower Salt/Lower Gila geographic area, the classification with Middle-Late

people from Northeastern Arizona/Zuni River can possibly be explained by migration and gene flow that occurred between these areas starting in the mid-thirteenth century.

Based on early excavations at several Hohokam Classic Period (AD 1150–1450) sites in the Phoenix Basin, Cushing inferred that the occupants of villages along the Salt River were ancestral to the contemporary Zuni people (Brunson 1989; Cushing 1890). More recent studies support that immigration into the Lower Salt/Lower Gila area from the north and west occurred AD 1050–1150 with an increase in population in the Phoenix Basin (Hill et al. 2004; Ingram 2008). For example, the Kayenta diaspora involved people moving from northeastern Arizona southward into occupied settlements in the Safford Basin, San Pedro Valley, and Tonto Basin (Clark 2001; Lyons 2003; Neuzil 2008; Woodson 1999). In the Phoenix Basin, possible Kayenta migrant and descendent enclaves were identified at Las Colinas and Los Muertos in the lower Salt River Valley (Haury 1945; Hill et al. 2015). Therefore, it is highly likely that the individual tested within this study had origins in the northern Southwest post-AD 1300, or was a descendant from people who did.

Many archaeologists think that modern Zuni culture was formed through the merging of Pueblo people from the northern Colorado Plateau and people from the south with different cultural traditions, such as groups from the Mogollon Highlands (Cushing 1896; Ferguson 1981; Watson et al. 1980; Woodbury 1979). During the Protohistoric transition (AD 1400–1450) Zuni town underwent drastic changes in settlement organization, architecture, ceramic design and technology, and mortuary practices (Ferguson 1996; Kintigh 2000; Peeples 2014). Two towns, Hawikku and Kechiba: wa, began practicing cremation and interring cremated remains in clusters, a practice that accounts for 30% of the burial features during this time (Kintigh 2000; 109). Matsaki Buff Ware was the most common ceramic ware associated with these cremations,

and was also found associated with inhumations. This ware was ubiquitous in the area until 1680, although other wares were also associated with cremations to a lesser degree, including Roosevelt Red Ware (Mills 2007). Kintigh (2000) suggests that these patterns are the result of either the diverse origins of the founding population in the Protohistoric villages or an uneven migration of new arrivals into the area. This is possibly due to an influx of people from southern and western locales known for practicing cremation, such as the Hohokam in the Lower Salt and Lower Gila River Valleys, and people from the Mogollon area. A direct connection is inferred between the Point of Pines area, in the central Arizona Mountains, and Zuni from shared specific cremation mortuary practices, vessel killing, and rim notching (Mills 2007; Robinson and Sprague 1965). Overall, protohistoric Zuni towns were dynamic and diverse as indicated in patterns of ceramic technology and mortuary practices.

Biological distance (biodistance) analysis of population structure, social network analysis, and oral tradition has further supported inferences connecting the southern Hohokam and Mogollon with the northern Zuni and Hopi cultural traditions. Peeples (2014) summarized previously available genetic data and found that there were significant levels of differentiation in earlier versus later samples from sites undergoing the Protohistoric transition in the Zuni area. Higher variance was found at Hawikku, which he interprets as external gene flow from outside of the Zuni region, although a close genetic relationship is also inferred among local groups. He also finds that prehistoric Zuni individuals (especially those from the earlier Pueblo II/III sites dating to AD 1000–1275) show close affiliation with Chaco Canyon, Sinagua (Central Arizona), and Lower Salt groups. The historic Zuni Halona:wa mission sample is most phenotypically similar to several sub-regional populations located in east-central Arizona, such as Grasshopper Pueblo, the Globe area, and the Puerco of the West (Peeples 2014). These findings support that

long distance migration occurred between the northern and southern portions of the Southwest during this time.

Social network analyses conducted in the Southwest have examined the strength of connectivity and network density among archaeological settlements through time. Mills and colleagues (2013) reveal that during AD 1250–1300, most Southwest sites are clustered in the northern portion of the region whereas after AD 1300 trajectories diverged in the south. New networks emerged in the south that were tied to Salado polychrome pottery and Kayenta migrants and their descendants that co-resided with locals in certain south-central Arizona settlements. However, by AD 1400, some areas such as the Phoenix Basin sites were densely occupied yet became increasingly isolated as population declined regionally. By AD 1450, the northern and southern portions of the Southwest region were essentially disconnected (Mills et al. 2013). Borck et al. (2015) examine degree of embeddedness and find that Hopi and Zuni settlements persisted longer than other pre-contact Southwest sedentary villages. However, whereas Hopi is inferred to have utilized external connections in the face of environmental crises, Zuni settlement population increased and became internally denser. Connections in these areas are possibly tied to a cycle of migration that began with the Kayenta diaspora and depopulation of the San Juan River drainage with people moving south by AD 1280, and then dispersal and return migration north into aggregated communities of Hopi and Zuni post-AD 1400 (Mills 2007).

Oral tradition is a line of evidence that also needs to be integrated with biological and archaeological evidence when establishing cultural affiliation (Echo-Hawk 2000). One example of connecting the Hopi and Hohokam cultural traditions, include Hopi oral tradition that says early Hopi clans spent time at *Palatkwapi* located far south from the Hopi Mesas, which has led

some Hopi clans to claim cultural affiliation with the Hohokam (Ferguson et al. 2003; Ferguson and Loma'omvaya 1999). Lineages, clans, kiva-groups, non-kin based moieties, and ritual sodalities are examples of sub-groups within cultural areas that, alongside migration, supported intragroup variation and heterogeneity across the region.

The results of the analysis, in conjunction with population histories reconstructed from multiple integrated lines of evidence, not only identify an individual as a possible migrant from the northern Southwest who died in the southern Southwest, but also support inferred migration trajectories between the Northeastern Arizona/Zuni River, Lower Salt/Lower Gila, and Arizona Mountains/Mogollon Highlands areas. This highlights the importance of emphasizing and integrating archaeological and social network interpretations of migration within future biological affiliation analyses to support cultural affiliation determinations.

Next, two cultural affiliation determinations conducted within the past decade represent real scenarios that emphasize how biological aspects of identity have largely been de-emphasized in Southwest cultural affiliation studies.

Cultural Affiliation Case Studies in the North American Southwest: Chaco Canyon

The cultural affiliation of human remains associated with archaeological sites from Chaco Canyon National Historical Park (CCNHP) faced intense scrutiny and critique. Multiple tribes, including the Hopi, Navajo, and the Pueblos of Acoma, Zia, and Zuni claimed cultural affiliation with the remains in the mid-1990s. These tribes agreed to consolidate repatriation requests, and that reburial would occur in the park. Published craniometric and mtDNA evidence was used to support cultural affiliation with the claimant tribes, including the Navajo Nation (Corruccini 1972; Hrdlička 1935; Lorenz and Smith 1996; Parr et al. 1996; Seltzer 1944).

Craniometric studies emphasizing biological continuity among Ancestral Puebloan groups in the San Juan and Rio Grande River drainages, specifically those with close morphological affiliation between individuals from Pueblo Bonito and Hawikku (Corrunccini 1972; Seltzer 1944) were inferred to emphasize population continuity with groups to the south and east. Previously conducted mtDNA analyses indicated that 2.1% of southwestern Athabaskan females in each generation originated from surrounding non-Athabaskan populations (Lorenz and Smith 1996; Parr et al. 1996), providing support for the conclusion that intermarriage and admixture occurred with Athabaskan-speakers when they entered and settled in the Southwest. The Chaco Canyon human remains and funerary objects were repatriated to the claimant tribes and reburied in 2006.

Cordell and Kintigh (2010) argue that the NAGPRA Review Committee (NRC) largely discredited the CCNHP's findings on cultural affiliation. They also state that sites with limited contextual information were treated as cultural affiliated with the claimant tribes and cultural affiliation was not made on a site-by-site basis. This decision was contested as research supports a southward Athabaskan migration into the Southwest approximately 500 years ago, whereas the 'Chaco World' was inhabited much earlier beginning around AD 800 through 1200 and was depopulated at least 200 years before the Athabaskan migration (Navajo and Apache) (Malhi et al. 2003; Seymour 2012). Methodological obstacles that physical anthropologists face include the limitations of biological units (i.e. gene pools, populations) that are needed to infer shared biological relatedness as skeletal remains recovered archaeologically are not representative samples of biological populations (Schillaci and Bustard 2010). This case highlights the complicated nature of integrating biological evidence into cultural affiliation studies in the Southwest US. By synthesizing a large representative craniometric database from the region,

more comprehensive morphological comparisons can be tested so that biological anthropologists rely less on broad, over-generalized historical craniometric analyses.

Cultural Affiliation and Repatriation at Fort Union, New Mexico

In the mid-1950's four inadvertently discovered co-located burials were recovered dating to 1862-1875, at the Fort Union National Monument, in northern New Mexico. The remains were transferred to the Museum of Northern Arizona, and an analysis of dental morphology was undertaken, and concluded that all four of these individuals exhibited markers of multiple ethnicities indicative of admixture. They were referred to as "Mexican," with the possibility of Athabaskan admixture (Turner 1960). Two additional biological studies followed. Fenton (1995) identified two of the Fort Union individuals as Native American, and reported that the other two exhibited morphological indications of admixture. Due to this discrepancy, a third ancestry analysis was commissioned.

Beck and McClelland (2005) inferred that two of the individuals were Native American, based on winging and shoveling of the maxillary incisors and facial features, and one was an admixed individual which agreed with Fenton's findings. However, based on subtense measurements and other morphological features they concluded that one was of European descent. These remains were repatriated as unaffiliated in 2007 to the Jicarilla Apache tribe. Spude and Scott (2013) suggest that that these were three Apache men, and one New Mexican Volunteer named Miguel Lucero, and this this individual was inappropriately repatriated to the Jicarilla Apache tribe. Although biological evidence is often available, additional work is needed to successfully integrate such evidence into cultural affiliation or cultural affinity determinations in the Southwest.

Conclusions

Biological evidence is one of the eleven lines of evidence that can be drawn upon to help establish cultural affiliation of human skeletal remains according to NAGPRA. Cranial morphology follows neutral microevolutionary patterns and morphometric analyses serve as a genetic proxy to help examine biological relatedness between archaeological skeletal samples and individuals with little or no contextual information designated as culturally unidentifiable and culturally unaffiliated. It is essential to follow the appropriate statistical procedures and test assumptions in order to achieve the most accurate, optimal results. Otherwise, using LDFA to this end could end up being misleading. Constructing regionally representative reference samples can help anthropologists more accurately use cranial morphological evidence in the cultural affiliation determination process. Furthermore, this tool can be used to help engage and consult with tribes, as it is essential to integrate biological, archaeological, and oral tradition evidence when reconstructing population histories needed to most accurately interpret biological affiliation results.

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FIGURE 1: Reference sample map

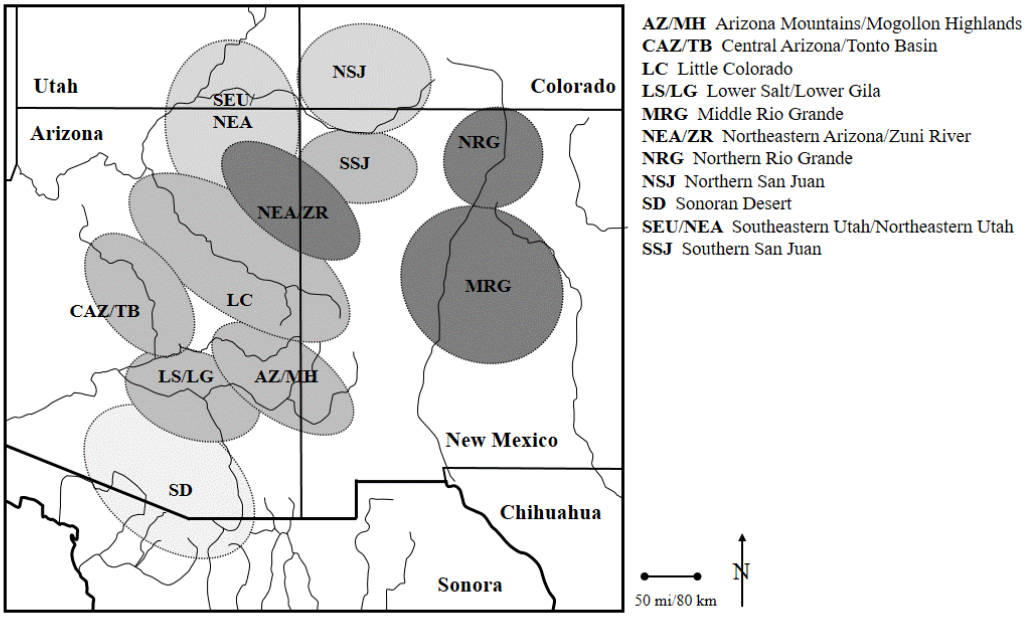

Figure 2: Cranial Measurement Diagram exhibiting craniofacial measurements included in the test individual analysis

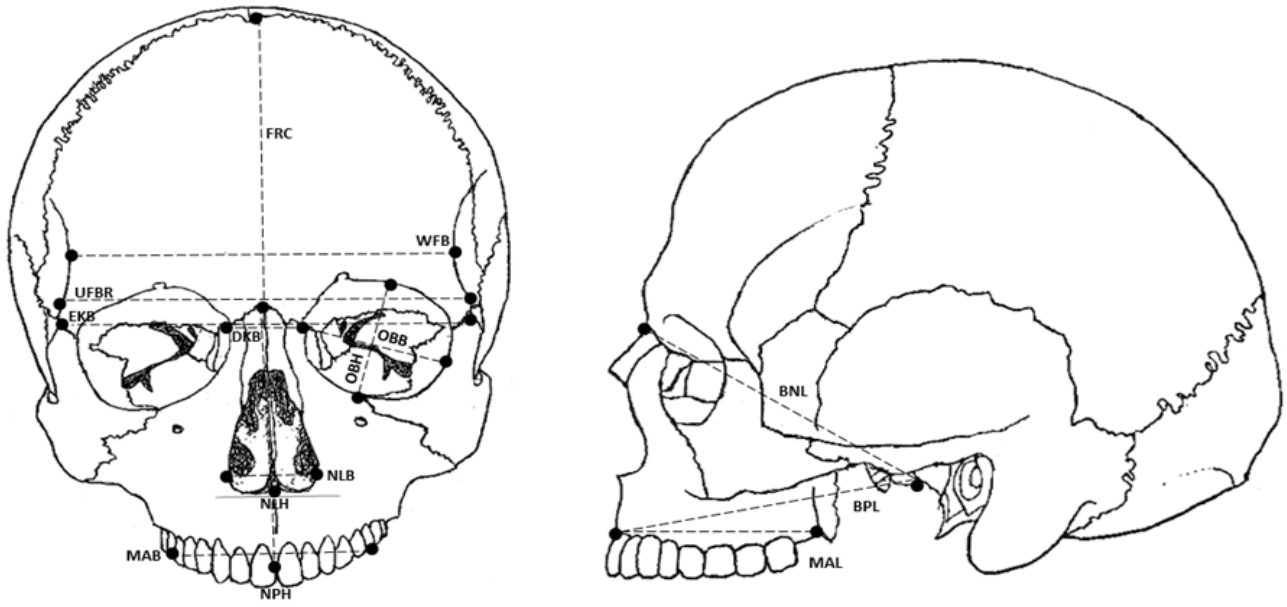

Figure 3: Canonical Variate Scatter plot showing classification of case study

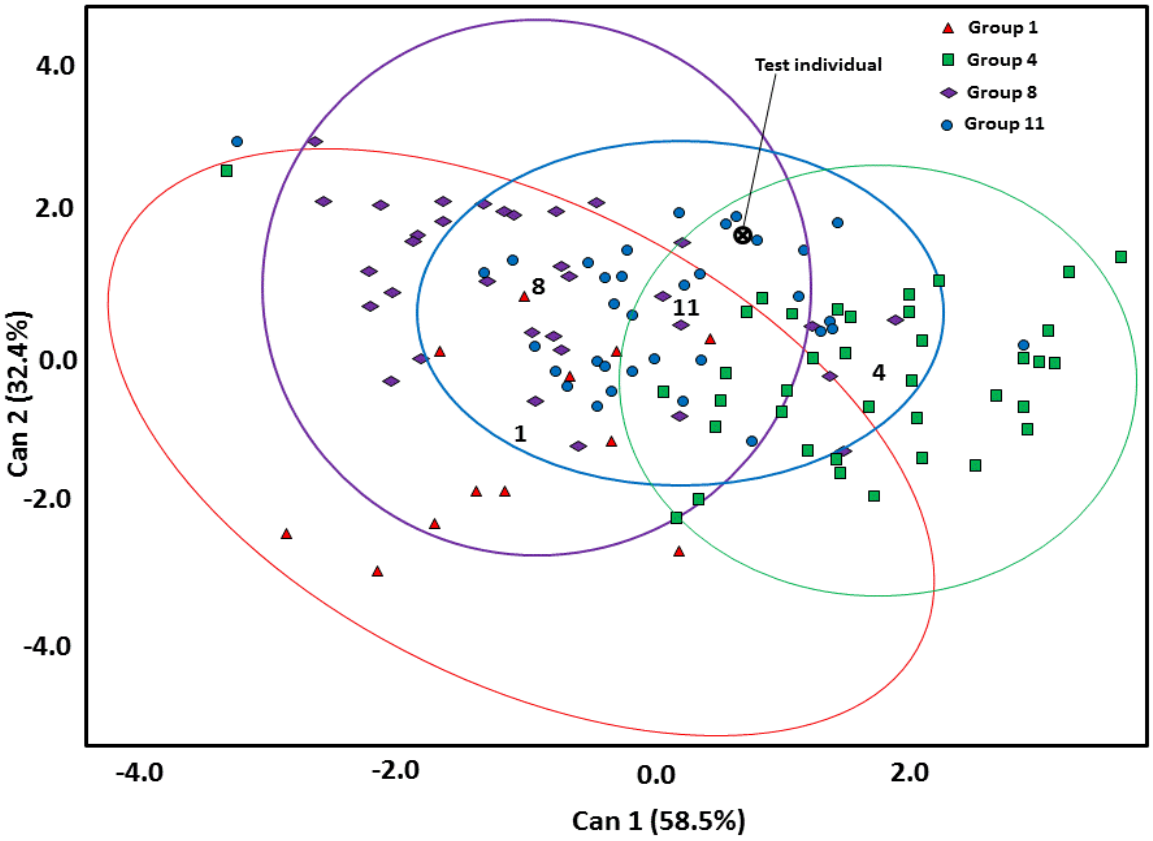

TABLE 1: Samples Table

Group No.	Code	Sub-region/site	Temporal Group	*n*
1	**SD**	Sonoran Desert	Early	69
2	**NSJ**	Northern San Juan	Early-Middle	199
3	**SEU/NEA**	Southeast Utah/Northeastern Arizona	Early-Middle	128
4	**SSJ**	Middle and Southern San Juan	Middle	128
5	**CAZ/TB**	Central Arizona/Tonto Basin	Middle	81
6	**LS/LG**	Lower Salt/Lower Gila	Middle	145
7	**LC**	Little Colorado	Middle	177
8	**MH**	Arizona Mountains/Mogollon Highlands	Middle	279
9	**NRG**	Northern Rio Grande	Middle-Late	223
10	**MRG**	Middle Rio Grande	Middle-Late	307
11	**NEA/ZR**	Northeastern Arizona/Zuni River	Middle-Late	105

TABLE 2: Description of measurements included in the analysis

No.	Code	Measurement Name	Description
1*	WFB	Minimum Frontral Breadth	Direct distance between the two frontotemporale
2	UFBR	Upper Facial Breadth	Direct distance between the two external points on the frontomalar suture
3*	EKB	Biorbital Breadth	Direct distance between right and left ectoconchion
4*	DKB	Interorbital Breadth	Direct distance between right and left dacryon
5*	NLH	Nasal Height	Direct distance from nasion to the midpoint of a line connect the lowest points of the inferior margins of the nasal notches
6*	NLB	Nasal Breadth	Maximum breadth of the nasal aperture
7*	OBH	Orbital Height	Direct distance between the superior and inferior orbital margins
8	OBB	Orbital Breadth	Lateral sloping distance from dacryon to ectoconchion (not necessarily at suture)
9*	MAL	Maxillo-Alveolar Length	Direct distance from prosthion to alveolon
10*	MAB	Maxillo-Alveolar Breadth	Maximum breadth across the alveolar borders of the maxilla measured on the lateral surfaces at the locaion of the secondary maxillary molars.
11	BPL	Basion-Prosthion Length	Direct distance from basion to prosthion
12	BNL	Basion-Nasion Length	Direct distance from nasion to basion
13	FRC	Frontal Chord	Direct distance from nasion to bregma
14	NPH	Nasion Prosthion Height	Direct distance from nasion to prosthion
15	GOL	Maximum Cranial Length	Distance between glabella and opisthocranion in the midsagittal plan, measured in a straight line
16	XCB	Maximum Cranial Breadth	Maximum width of skull perpendicular to midsagittal plan wherever it is located, with the exception of the inferior temporal lines and the area immediately surrounding them.
17	BBH	Basion-Bregma Height	Direct distance from the lowest point on the anterior margin of forament magnum to bregma
18	AUB	Biauricular Breadth	Least exterior breadth across the roots of the zygomatic processes
19	ZYB	Bizygomatic Breadth	Direct distance between most lateral points on the zygomatic arches
20	PAC	Parietal Chord	Direct distance from bregma to lambda
21	OCC	Occipital Chord	Direct distance from lambda to opisthion
22	FOL	Foramen Magnum Length	Direct distance from basion to opisthion
23	FOB	Foramen Magnum Breadth	Distance between the larteral margins of forament magnum at the points of greatest lateral curvature

* measurement included in the test individual analysis

TABLE 3: Consultation recommendations based on reference group biological affiliation

Biologically Affilliated Group	Federally-Recognized Tribe to Consult	State
6	Ak Chin Indian Community of Maricopa (Ak Chin)	AZ
5; 6; 7; 8	Salt River Pima-Maricopa Indian Community of the Salt River Reservation	AZ
1; 6	Tohono O'odham Nation of Arizona	AZ
1; 3; 5; 7; 8	Fort McDowell Yavapai Nation	AZ
5	Fort Mojave Indian Tribe	AZ
6	Gila River Indian Community of the Gila River Indian Reservation	AZ
1; 2; 3; 4; 5; 6; 7; 8; 9; 10; 11	Hopi Tribe of Arizona	AZ
2; 4; 5; 7; 8	Navajo Nation	AZ, NM, UT
1; 6	Pascua Yaqui Tribe of Arizona	AZ
1	San Carlos Apache Tribe of the San Carlos Reservation	AZ
1; 5; 6; 7; 8	Tonto Apache Tribe of Arizona	AZ
5; 6; 7; 8	White Mountain Apache Tribe of the Fort Apache Reservation	AZ
1; 5; 6	Yavapai-Apache Nation of the Camp Verde Indian Reservation	AZ
5	Yavapai-Prescott Indian Tribe	AZ
3	Southern Ute Tribe of the Southern Ute Reservation	CO
3	Ute Mountain Tribe of the Ute Mountain Reservation	CO, NM, UT
2; 4; 9; 10	Pueblo of Ohkay Owingeh	NM
2; 3; 4; 9; 10; 11	Pueblo of Acoma	NM
2; 4; 9; 10	Pueblo of Cochiti	NM
2; 4; 9; 10	Pueblo of Jemez	NM
2; 4; 9; 10	Pueblo of Isleta	NM
2; 3; 4; 9; 10	Pueblo of Laguna	NM
2; 4; 9; 10	Pueblo of Nambe	NM
2; 4; 9	Pueblo of Picuris	NM
2; 4; 9; 10	Pueblo of Pojoaque	NM
2; 4; 9; 10	Pueblo of San Felipe	NM
2; 4; 9; 10	Pueblo of San Ildefonso	NM
2; 4; 9; 10	Pueblo of Sandia	NM
2; 4; 9; 10	Pueblo of Santa Ana	NM
2; 4; 9; 10	Pueblo of Santa Clara	NM
2; 4; 9; 10	Kewa Pueblo	NM
2; 4; 9	Pueblo of Toas	NM
2; 4; 9; 10	Pueblo of Tesuque	NM
2; 4; 9; 10	Pueblo of Zia	NM
1; 2; 3; 4; 5; 6; 7; 8; 9; 10; 11	Zuni Tribe of the Zuni Reservation	NM

TABLE 4: Case study typicality and posterior probabilities

Group	Classified into	Distance from	Posterior	Typ F	Typ Chi	Typ R	Correct
1		13.2	0.007	0.199	0.106	0.154	58.3.%
4		8.1	0.088	0.891	0.865	0.649	83.30%
8		6.5	0.196	0.501	0.424	0.405	60.60%
11	**11**	3.9	0.709	0.658	0.593	0.706	66.70%

SUPPLEMENTARY MATERIALS: TABLE 1: Complete reference groups with analysts and sources of data

Group No.	Sub-region/site	Temporal Group	*n*	Analyst	Source
1	**Sonoran Desert**	**Early**	**69**		
	Donaldson AZ EE:2:30		5	RB	collected by author
	Los Ojitos AZ EE:2:137		5	RB	collected by author
	La Playa SON F:10:3		37	RB	collected by author
	Las Capas AZ AA:12:111		6		ASM Bioarchaeology Lab
	Los Pozos AZ AA:12:91		3		ASM Bioarchaeology Lab
	Santa Cruz Bend AZ AA:12:90		1	PM	Minturn et al. 1998
	Ventana Cave		10		ASM Bioarchaeology Lab
	Wetlands		2	LB	Guthrie and Lincoln-Babb 1998
2	**Northern San Juan**	**Early-Middle**	**199**		
	Falls Creek		5	DM	collected by author
	Talus Village		4	DM	collected by author
	Ignacio Field Camp		1	F&W	Fenega and Wendorf 1956
	Tammarron		1	EKR	Reed and Kainer 1978
	Ridges Basin (5LP238, 5LP0171; 5LP0176; 5LP0184; 5LP0185; 5LP0237; 5LP0245; 5LP0246; 5LP0511)		23	AS	Stodder 2010
	Bodo Canyon (5LP481; 5LP483)		3	DM	collected by author
	West Animas		1	AS	Stodder 2010
	5MT10010; 5MT10991; 5MT2182; 5MT2848; 5MT4475; 5MT4684; 5MT4725; 5MT5106; 5MT5107; 5MT5108; 5MT7704; 5MT8899; 5MT8943; 5MT9541; 5MT9924; 5MT9924; 5MT9934; 5MT9942; 5MT9943; 5MT10207; 5MT1020; 5MT7723; 5MT2192; 5MT2320; 5MT2336; 5MT4477; 5MT4545; 5MT4671; 5MT:--		43	AS	Stodder 1987
	5MV80; 5MV1241; 5MV1253; 5MV866		4	KB	Ortman 2010
	Ackmen		6	BL	Ortman 2010
	Arboles Area		1	DEM	collected by author
	Badger House		3	KB	Matthew Peeples, personal communication
	Big Juniper House		3	KB	Matthew Peeples, personal communication
	Cliff Dweller		8	BL	Ortman 2010
	Dog House MV1676		1	KV	Ortman 2010
	Wallace		5	CJB	Ortman 2010
	Coyote Village		2	DEM	Ortman 2010

	Dominguez		1	LJS	Ortman 2010
	Navajo Reservoir (LA4131; LA4151; LA4769; LA4195; LA4198; LA4242)		15	KB; EKR	Bennett 1966; Reed 1966
	Lister Site 1, 2		2	DEM	Ortman 2010
	Long House		9	KB	Matthew Peeples, personal communication
	Lowry		7	BL	Ortman 2010
	Mancos Canyon		1	BL	Ortman 2010
	Montezuma Canyon		5	AH	Ortman 2010
	Mug House		7	KB	Matthew Peeples, personal communication
	MV Museum; Mesa Verde (no ID)		12	KB	Matthew Peeples, personal communication
	Sand Canyon Pueblo		3	DEM	Ortman 2010
	Site 1241; 1253; 1676; 34		14	KB	Matthew Peeples, personal communication
	Soda Canyon Pueblo		3	DEM	Ortman 2010
	Two Raven House		6	KB	Ortman 2010
3	**Northeastern Arizona/Southeast Utah**	**Early-Middle**	**128**		
	Black Mesa		24	RB	collected by author
	Inscription House		7	EKR	Matthew Peeples, personal communication
	Kaibito Road		1	EKR	Matthew Peeples, personal communication
	Keet Seel		2	EKR	Matthew Peeples, personal communication
	Sayodneechee Cave		5	DM	collected by author
	White Dog Cave		3	DM	collected by author
	Glen Canyon, Sand Dune Cave		1	AL	Lindsay Jr. et al. 1968
	Graham Canyon		1	BL	Ortman 2010
	Grand Gulch		68	AH	Hrdlicka 1931
	Site 5; 8; 12; 13		12	AB	Ortman 2010
	42SA7005; 42SA738		4	EKR	Ortman 2010
4	**Southern San Juan**	**Middle**	**128**		
	299; 396; 563; 577; 627; 721; 1360; 9999; 1947; 9090; 2999		35	NJA	Ortman 2010
	Bc 362; Bc 59		5	EKR	Ortman 2010
	Kin Kletso		1	EKR	Ortman 2010
	Pueblo del Arroyo		1	EKR	Ortman 2010
	Pueblo Bonito		46	MS	Michael Schillaci, personal communication
	LA 3292; LA37592; LA 37601; LA 65030		8	MS	Ortman 2010
	Aztec		12	MS	Michael Schillaci, personal communication
	Lone Kiva Site		2	MG	Ortman 2010
	Mine Canyon Site		7	MG	Ortman 2010
	Salmon		3	MG	Ortman 2010

	Tommy Site		8	MG	Ortman 2010
5	**Central Arizona/Tonto Basin**	**Middle**	**81**		
	Elden Pueblo		18	AH	Hrdlicka 1931
	King's Ruin		7	JW	collected by author
	McGoonie Site AZ O:12:25		2	PM	Matthew Peeples, personal communication
	Whitlow Ranch AZ O:12:38		8	PM	Matthew Peeples, personal communication
	AZ U:3:294; AZ U:3:297; AZ U:3:298; AZ U:3:299; AZ U:3:405; AZ U:3:5; AZ U:4:32; AZ U:4:33; AZ U:4:7; AZ V:5:119		43	PM	Matthew Peeples, personal communication
	Shoofly Village		3	PM	Matthew Peeples, personal communication
6	**Lower Salt/Lower Gila**	**Middle**	**145**		
	Las Acequias		6	PM	Matthew Peeples, personal communication
	Los Muertos		123	AH	Hrdlicka 1931
	Togetzoge		10	MS	Michael Schillaci, personal communication
	San Simon Village		6	AMB	Matthew Peeples, personal communication
7	**Little Colorado**	**Middle**	**177**		
	Black Falls		7	AH	Hrdlicka 1931
	Chaves Pass		37	AH	Hrdlicka 1931
	Chevlon		4	AH	Hrdlicka 1931
	Four Mile Canyon		9	AH	Hrdlicka 1931
	Kin Tiel		10	AH	Hrdlicka 1931
	Petrified Forest		18	AH	Hrdlicka 1931
	Wupatki		7	B&S	Matthew Peeples, personal communication
	Allentown		9	JW	collected by author
	Manuelito		5	AH	Hrdlicka 1931
	Pueblo de los Muertos		6	LS	Ortman 2010
	Quemado		3	JW	collected by author
	Slade Ruin		35	JW	collected by author
	Techado Spring		7		Matthew Peeples, personal communication
	Village of the Great Kivas		8	MS	Ortman 2010
	Whitewater		10	TDS	Ortman 2010
	Whitewater Arroyo		2	AH	Hrdlicka 1931
8	**Mogollon Highlands**	**Middle**	**279**		
	Grasshopper Pueblo		154	RB	collected by author
	Point of Pines Pueblo		48	RB	collected by author
	Turkey Creek Pueblo		29	RB	collected by author
	Kinishba		40	TB	ASM Bioarchaeology Lab
	LA635; LA676; LA15044; LA15075; LA12076; LA70163		8	MS	Michael Schillaci, personal communication

9	**Northern Rio Grande**	**Middle-Late**	**223**		
	Agua Fria		1	MS	Ortman 2010
	Arroyo Hondo		13	EO, AMP	Ortman 2010
	Burnt Mesa Pueblo		1	MN	Ortman 2010
	LA641; LA3558; LA742; LA103979E; LA103919W; LA3643; LA391		12	EKR	Ortman 2010
	Johnson Pit House		2	EKR	Ortman 2010
	Kwahe'e		2	EKR	Ortman 2010
	Largo Canyon		2	JW	collected by author
	Otowi		17	MS	Michael Schillaci, personal communication
	Puye		47	MS	Michael Schillaci, personal communication
	Picuris		7	MS	Michael Schillaci, personal communication
	Pindi		18	MS	Michael Schillaci, personal communication
	Ponsipa'akeri Pueblo		1	JW	collected by author
	Poshuouinge		2	AH	Ortman 2010
	Pot Creek		10	MS	Michael Schillaci, personal communication
	San Cristobal		41	MS	Michael Schillaci, personal communication
	Sapawe		17	MS	Michael Schillaci, personal communication
	TA47		3	MS	Ortman 2010
	Taos		2	MS	Michael Schillaci, personal communication
	Te'ewi		9	EKR	Michael Schillaci, personal communication
	Tsankawi		3	AH	Hrdlicka 1931
	Tsirege		11	AH	Hrdlicka 1931
	Yunque		2	EKR	Ortman 2010
10	**Middle Rio Grande**	**Middle-Late**	**307**		
	Amoxiumqua		7	MS	Ortman 2010
	Giusiwa		8	AH	Hrdlicka 1931
	Kwasteyukwa		33	AH	Hrdlicka 1931
	Paa-ko		23	SLR	Ortman 2010
	Pecos Pueblo		97	EH	Hooten 1930
	Pottery Mound		24	MS	Michael Schillaci, personal communication
	Tijeras		5	DSW	Ortman 2010
	LA25; LA70; LA183; LA3333; LA6455; LA9154		49	MS, MOS	Ortman 2010
	Gran Quivira		57	EKR	Reed 1981
	Pueblo Largo LA183		4	JW	collected by author
11	**Northeastern Arizona/Zuni River**	**Middle-Late**	**105**		
	Atsinna		1	AH	Hrdlicka 1931

Hawikku	46	JW	collected by author
Heshotauthla	22	MS	Ortman 2010
Old Zuni Church/Halona:wa Mission	26	EKR	Ortman 2010
Sikyatki	3	AH	Hrdlicka 1931
Tsegi	1	EKR	Matthew Peeples, personal communication
Homolovi	1	AH	Hrdlicka 1931
Awatobi	5	AH	Hrdlicka 1931

SUPPLEMENTARY MATERIALS: TABLE 2: List of analysts contributing data included in this study

Analyst Initials	Analyst Name
AH	Ales Hrdlička
AL	Alexander Lindsay Jr.
AS	Ann Stodder
B&S	Baily and Schurr
BL	Brian Lesley
CB	Cindy Bradley
DM	Dawn Mulhern
DEM	Debra Martin
EO	Eric Ozolins
ER	Erik Reed
F&W	Fenga and Wendorf
FS	Floyd Sharrock
JW	James Watson
KB	Kenneth Bennet
LLB	Lorrie Lincoln-Babb
LS	Linda Smith
MD	Michael Dice
MG	Michelle Greene
MS	Michael Schillaci
NA	Nancy Akins
PL	Patricia Lambert
PM	Penny Minturn
R&W	Reed and Kainer
RB	Rachael Byrd
SU	Sally Underwood
TB	Theodora Burbank
TDS	T.D. Stewart